

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:43:37 ; Search time 13.5644 Seconds
(without alignments)
1545.568 Million cell updates/sec

Title: US-09-911-777-1

Perfect score: 1116

Sequence: 1 MDDSTERQSRITSLCKRE.....ENAIQLDGDVTFGALKLL 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	8.2	1121	2 S57058	probable membrane
2	88	7.9	664	1 WMBEBH	infected cell prot
3	87.5	7.8	240	1 S76714	hypothetical prote
4	85	7.6	213	2 C81874	hypothetical prote
5	84.5	7.6	637	2 S36523	E1 protein - human
6	84	7.5	563	2 F95076	sensor histidine k
7	84	7.5	563	2 C97944	histidine kinase (
8	83.5	7.5	360	2 G64575	conserved hypothet
9	83.5	7.5	596	2 B96834	hypothetical prote
10	83.5	7.5	630	1 W1WL35	E1 protein - human
11	83	7.4	218	2 D81148	conserved hypothet
12	82.5	7.4	228	2 T01350	hypothetical prote
13	82.5	7.4	737	1 K1PTCE	protein kinase C (
14	82	7.3	620	2 JH0821	95K golgi antigen
15	81.5	7.3	737	1 K1MSCE	protein kinase C (
16	81.5	7.3	760	2 S55520	chitin synthase (E
17	80.5	7.2	325	2 S35303	superantigen Mtv -
18	80.5	7.2	330	2 B43307	phosphoprotein pho
19	79.5	7.1	330	2 F75410	conserved hypothet
20	79	7.1	533	2 F75583	GGDEF family prote
21	78.5	7.0	330	2 T47576	FKBP12 interacting
22	78	7.0	233	2 S11688	tumor necrosis fac
23	78	7.0	233	2 T02390	citrate (ci)-synth
24	78	7.0	1655	2 T13998	gene mastermind pr
25	77.5	6.9	320	2 S26387	superantigen Mtv9
26	77.5	6.9	320	2 AF3237	transcriptional re
27	77.5	6.9	356	2 B30338	late competence pr
28	77.5	6.9	889	2 B55123	coatamer complex b
29	77	6.9	431	2 S56228	alpha-factor recep

30 77 6.9 665 2 E82506
31 76.5 6.9 737 1 S28942
32 76.5 6.9 877 1 A25962
33 76.5 6.9 1208 2 A31947
34 76 6.8 378 1 OKGARI
35 76 6.8 473 2 D83246
36 76 6.8 592 2 C70302
37 76 6.8 674 2 T19268
38 76 6.8 1675 2 T31473
39 75.5 6.8 510 2 D69946
40 75.5 6.8 531 2 T30167
41 75.5 6.8 561 2 S71597
42 75.5 6.8 899 2 S76449
43 75.5 6.8 1490 2 T16086
44 75 6.7 278 2 T46458
45 75 6.7 672 2 H86169

ALIGNMENTS

RESULT 1

S57058

probable membrane protein YJR039w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein J1614

C/Species: Saccharomyces cerevisiae

C/Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 19-Apr-2002

C/Accession: S57058; S63780

R/Huang, M.E.; Chuat, J.C.; Galibert, F.

submitted to the Protein Sequence Database, September 1995

A/Reference number: S57052

A/Accession: S57058

A/Molecule type: DNA

A/Residues: 1-1121 <MAN>

A/Cross-references: EMBL:Z49538; NID:gl015687; PID:gl015689; MIPS:YJR039w

R/Huang, M.E.; Chuat, J.C.; Galibert, F.

Yeast 11, 775-781, 1995

A/Title: Analysis of a 42.5 kb DNA sequence of chromosome X reveals three tRNA genes and

A/Reference number: S63757; MUID:95397595; PMID:7668047

A/Accession: S63780

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-1121 <HUA>

A/Cross-references: EMBL:L36344

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996

A/Cross-references: SGD:S0003800

A/Map position: 10R

A/Note: YJR039w

C/Superfamily: Saccharomyces cerevisiae probable membrane protein YJR039w

C/Keywords: transmembrane protein

Query Match 8.2%; Score 91; DB 2; Length 1121;
Best Local Similarity 25.3%; Pred. NO. 4;
Matches 39; Conservative 22; Mismatches 51; Indels 42; Gaps 8;

QY 15 CLKREKNKLCVCYSILPKRSPSVLLSCCLTVVSFYQVAALQGLASLRAELQSHH--A 72

DB 155 CLEE--TDVKLSYVTS-----SPIVSDACINFNDF-----LDKDVFTLSILTRAHNEVA 202

QY 73 EKLPAKAGIFPPAPGEGNSQNSRNRKAVQGPETVTQDCLQLIADSETPTIQKGSYTF 132

DB 203 YKLEACVCFE--SRPAKTKWQRTNLTFFE--EATVSQVLLKSVTNL-----GHFVF 252

QY 133 VPWLLSFKRGSAIXQVLYTDKTYAMGHLIQRKK 166

DB 253 TPW-----KTVFIKHALSSKQ 268

RESULT 2

WMBEBH

infected cell protein ICP18.5 - bovine herpesvirus 2 (strain BMV)

C:Species: bovine herpesvirus 2
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Nov-1996
C:Accession: B29242
R:Hammerschmidt, W.; Contraths, F.; Mankertz, J.; Pauli, G.; Ludwig, H.; Buhk, H.J.
Virology 165, 388-405, 1988
A:Title: Conservation of a gene cluster including glycoprotein B in bovine herpesvirus 2
A:Reference number: A94381; MUID:88306231; PMID:2841793
A:Accession: B29242
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-664 <HAM>
A:Cross-references: GB:M21628
C:Superfamily: herpesvirus infected cell protein ICPI8.5
C:Keywords: capsid assembly

Query Match 7.9%; Score 88; DB 1; Length 664;
Best Local Similarity 23.5%; Pred. No. 4.1;
Matches 46; Conservative 33; Mismatches 49; Indels 68; Gaps 11;

QY 29 SILPRKESPSVLLSCC---LTVVSFVQVAALQ-GDLASLRAELQGHAEKLPAGAKIFEP 84
DB 394 SAAPDDQIEALVACVNHLSAPVRLQAGSEHGDAELRSALGLHAEADP----- 445
QY 85 PAPGEGNSQSNRKRKAV-QGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGS 143
DB 446 --PGDGAKEARRAPSLGGPDE-----DWAALAAARAA 477
QY 144 ALYG--QVLYDTKTVMGHILQKVVHFGDELSTVLFRCIQNLSEGEDELQALPRENA 201
DB 478 ADVGARRRLYADR-----LTKR-----SLASLGRVCR--EORGELEKML----- 514
QY 202 QISLDGCV--TFEGAL 215
DB 515 RVSTYGEVLPVFAAV 530

RESULT 3
S76714
hypothetical protein - Synecocystis sp. (strain PCC 6803)
C:Species: Synecocystis sp.
A:Variety: PCC 6803
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: S76714
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76714
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-240 <KAN>
A:Cross-references: EMBL:D64004; GB:AB001339; NID:g1001701; PID:g1208490
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Start codon: GTG
C:Superfamily: conserved hypothetical protein MTH1849

Query Match 7.8%; Score 87.5; DB 1; Length 240;
Best Local Similarity 22.8%; Pred. No. 1.3;
Matches 52; Conservative 27; Mismatches 74; Indels 75; Gaps 10;

QY 1 MDDSTERQSRLLTSLCKREKNLKECVSILPRKESPSVLLSCCLTVVSFVQVAALQDGL 60
DB 1 MEPOGERNVGAIRAMK---NMGLEELVNP-----C-----DY 33
QY 61 ASLRAELQGHAEKLPAGAKIFEPAPGEGNSQ---NSRNKRAVQGPETVTQDCLQLI 117
DB 34 RSVEAQTWAVHAKVDVLAQAKVDDLTALGQRQRIATISARERILQSPMETPRQ----- 87
QY 118 ADSETPTIQKGSYTFVPWLLSFKRGSAL-YGQ--VLYTDKTYAMGHILQKVVHFGDEL 174

DB 88 -----ALPWLAPNLKLSALVFGREDSGLTNEELNQAHFRVRIPVHQPYPSSL 133
QY 175 SL-----VTLPRCIQ-----NLEEGDELQALPRENAQI 203
DB 134 NLSQAVWCVTYELLYQASLAMEYNNQVPGDRLEDGSTWPLA---TNAQL 178

RESULT 4
C81874
hypothetical protein NMA1086 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: C81874
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: C81874
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-213 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CA884349.1; PID:g737974
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1086

Query Match 7.6%; Score 85; DB 2; Length 213;
Best Local Similarity 22.9%; Pred. No. 1.9;
Matches 43; Conservative 30; Mismatches 63; Indels 52; Gaps 8;

QY 72 AEKLPA-GAKIFEPAPGEGNSONS-----RNKRAVQGPET--- 108
DB 23 SEQVARGVAVINHPNPLQGTNTNKVIQTAALKSLKGLPHYLPNLRGVGSGETHDYG 82
QY 109 --VTQDCLQLI-----ADSETPTIQKGSYTFVPWLLSFKRGSALYGOVL-----YTD 153
DB 83 RGETQDCLAVIDYARAQHPAEPALSGFSGGVVATFAAQARIPDLLLLIGAAVCHVTG 142
QY 154 K--TYAMGHILQKVVHFGDELSTVLFRCIQNLSEGEDELQALPRENAQISLDGDTVF 211
DB 143 RPEPSAVPNVAKTLMIHGADEV-----VEIGKALKWAEPQDLPVITIASGTHF 191
QY 212 F-GALKLL 218
DB 192 FHGKLIVL 199

RESULT 5
S36523
E1 protein - human papillomavirus type 35H
C:Species: human papillomavirus type 35H
C:Date: 09-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 26-Aug-1999
C:Accession: S36523
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36523
A:Molecule type: DNA
A:Residues: 1-637
A:Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52563.1; PID:g397000
A:Experimental source: strain 35H
C:Superfamily: papillomavirus E1 protein
C:Keywords: early protein; nucleus

Query Match 7.6%; Score 84.5; DB 2; Length 637;
Best Local Similarity 29.6%; Pred. No. 8.2;
Matches 45; Conservative 16; Mismatches 56; Indels 35; Gaps 8;

QY 19 REEMKLEKCVSILPRKESPSVLLSCCLTVVSFVQVAALQDGLASLRAELQGHAEKLPAG 78
DB 74 QEQTHKEAVQVLRKYVASPLSGSVSLCVNN-----NISPLKAICIKENKNTA 121

[illegible]

Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Bordovsky, M.; Karpk, P.D.; Smith, H.O.; F...
A>Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*
A;Reference number: A64520; MUID:97394467; PMID:95252185
A;Accession: G64575
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A;Residues: 1-360 <TOM>
A;Cross-references: GB:AE000560; GB:AE000511; NID:g2313554; PIDN:AAD07514.1; PI...
C:Genetics:
A;Start codon: GTG.

Query Match 7.5%; Score 83.5; DB 2; Length 360;
Best Local Similarity 24.08; Pred. No. 5.1;
Matches 56; Conservative 28; Mismatches 106; Indels 43; Gaps 11;

Qy 1 MDSTREQRRLTSCLKREEMKLKECVSILPKRSPSVLLSCSLTVVVSFYQVAALQGLD 60
Db 116 LEPSDAOAPEIKALKDSMFKKIKRAAKI.KELDGK---ECFITINMOYGMHPLAGEL 171

Qy	61	A-----SFAELQGHABKLP-AGAKIFEPAPAGEGNSQNSRNRKAVQG-----	104
Db	172	VSDVFYKPHNESPE\$PLK\$GKHLSEK\$PPKHLRVLD-NKPLAWIDV\$KESKEKRNADG\$Y\$YR	230
Qy	105	-PRETVTODCLOLIANSETIQKGSVTFVPWLL\$FKRGSALYCOVLYTDKTYAMGHLIQ	163
Db	231	ESBITAKCELDLFMKDE-PDFTFGVITF-----F\$EQKRLLEQAL-----KGYAN--LE	277
Qy	164	RKVHVVP-GBEL\$VLTVLFRCIQNLEEG-----DELQLAIPRENAQISLDGD	208
Db	278	IGTVDSFQGEFDV\$VFLSV\$VRHT\$EGFGLKISSCLCVALSQKRALIVAGD	330
RESULT 9			
B96834			
hypothetical protein F5f6.2 [imported] - Arabidopsis thaliana			
C/Species: Arabidopsis thaliana (mouse-ear cress)			
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001			
C/Accession: B96834			
R:Rheologics, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.			
Chin. C.W.; Chung, M.K.; Conn, L.; Conn, A.B.; Conway, A.R.; Creasy, T.H.; D			

ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzwerg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96834
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-596 <STO>
A:Cross-references: GB:AE005173; NID:g6751702; PIDN:AAF7684.1; GSPDB:GN00141
C:Genetics:
A:Gene: F516.2
A:Map position: 1

Query Match 7.5%; Score 83.5; DB 2; Length 596;
Best Local Similarity 19.3%; Pred. No. 9.4;
Matches 47; Conservative 42; Mismatches 97; Indels 57; Gaps 8;

Qy 12 LTSLCKREEMKLCVSIILPK-----EPPSVLLSCLTVVSYVAALQGDLS 62
Db LSKVLRRTQRLGACSAVFSKDIQLGERSFDSNSIASTKREAVPRFYEISLSNRALS 63
Qy 63 LRAELQGHAE-KLPAGAKIPFPAPGEGNSNSQNSKRAVQGPETVTQDCLQIADSE 121
Db 64 SAGATKQDEEDLDEGFSELGSKSGQGSTSDDEKLSADEEBELDLIE--TDVS 121
Qy 122 TPTIQGSYTFVPWLLS---FKRGSAlyGVLYTDKTYAMGH-----LIQRKVVH 168
Db 122 RKTVEKQSELFTKTVSAPGLSIGAL-----DKWVEEGNEITRVEIAKMLQRRR 174
Qy 169 VFG-----DELSVTLFRCTONLEEGDELOLAIPRENAQISLQGD 208
Db 175 MYGRALOMSEWLEANKKIEMTERDYASRLDITVKIRGLEKACQKIPK-----SPKGE 229
Qy 209 VTF 211
Db 230 VLY 232

RESULT 10
W1WL35
E1 protein - human papillomavirus type 35
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
R:Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillo
A:Reference number: A40824; MUID:92124753; PMID:1310198
A:Accession: A40824
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-630 <MAR>
A:Cross-references: GB:M74117; NID:g333050; PIDN:AAA46968.1; PID:g333053
C:Superfamily: papillomavirus E1 protein
C:Keywords: early protein

Query Match 7.5%; Score 83.5; DB 1; Length 630;
Best Local Similarity 29.6%; Pred. No. 10;
Matches 45; Conservative 15; Mismatches 57; Indels 35; Gaps 8;

Qy 19 REEMKLEKCVSLPRKESPVLLSCLTVVSYVAALQGDLSRAELQGHAEKLPAG 78
Db 73 QEEQTHKEAVQVLEKYASSPLSSVSLCVNN-----NISPLKALCIENKNTA 120
Qy 79 AK--IFEPAPGEGNSNSKRAVQGPETVTQDCLQIADSE-----ETPT-- 124
Db 121 AKRRLFELPDSGYGNSVEIHEIQVEG-HDTVEQ-CSMGSGDSITSSSDRHDPTPRD 178

ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzwerg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96834
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-596 <STO>
A:Cross-references: GB:AE005173; NID:g6751702; PIDN:AAF7684.1; GSPDB:GN00141
C:Genetics:
A:Gene: F516.2
A:Map position: 1

Qy 125 ---IQGSYTFVPWLLSFKRGSAlyGVLYTD 153
Db 179 IIQLKCSNANAMLAKEKE---LFG-LSFTE 206

RESULT 11
D81148
conserved hypothetical protein NMB0868 [imported] - Neisseria meningitidis (strain MC58
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: D81148
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: D81148
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-213 <TET>
A:Cross-references: GB:AE002439; GB:AE002098; NID:g7226100; PIDN:AAF41279.1; PID:g722610
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0868

Query Match 7.4%; Score 83; DB 2; Length 213;
Best Local Similarity 23.4%; Pred. No. 3;
Matches 44; Conservative 29; Mismatches 63; Indels 52; Gaps 9;

Qy 72 AEKLPK-AKATFEPPAPGEGNSNS-----RNKRAVQGPET--- 108
Db 23 SEQPARGVAVINHPNPLQGTNTNKVIQTAAKSLGHCYLPNLRGVGSGGTHDYG 82
Qy 109 --VTQDCLQLI-----ADSETPTTQKSYTFVPWLLSFKRGs-----ALYGOVL---YTD 153
Db 83 RGETQDCLAVIDYARAQHPAPEALSGFSFGGVATFAAQARTPDLLLLIGAACHVYTD 142
Qy 154 K--TYAMGHILQKVVHVGDELSTLTLFRCTONLEEGDELOLAIPRENAQISLQGDVTF 211
Db 143 RPEPSAVPNVAKTLMIHGADEV-----VEIGKALKWAEPODLPVITTAGSTHF 191
Qy 212 F-GALKLL 218
Db 192 FHGKLIVL 199

RESULT 12
T01350
hypothetical protein F6N15.4 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 14-May-1999
A:Accession: T01350
R:Ryan, E.; Edwards, J.; Pape, K.
submitted to the EMBL Data Library, May 1998
A:Description: The sequence of A. thaliana F6N15.
A:Reference number: Z14297
A:Accession: T01350
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-228 <RYA>
A:Cross-references: EMBL:AF069299; NID:g3193311; PID:g3193318
A:Experimental source: cultivar Columbia
C:Genetics:
A:Introns: 103/3
A:Map position: 4
A:Note: F6N15.4

Query Match 7.4%; Score 82.5; DB 2; Length 228;
Best Local Similarity 25.1%; Pred. No. 3.6;
Matches 46; Conservative 23; Mismatches 63; Indels 51; Gaps 9;

18 KREEMKLEKCVSILPRKESPSVLLSCCLTVVSF-YQVAALQGLDLSRAELQGHAEKLP 76
19 REEMKLEKCVSILPRKESPSVLLSCCLTVVSF-YQVAALQGLDLSRAELQGHAEKLP 76
70 KPDVAVSICFEAQLRDP--IYGVSHVLSQQOVSLOTLSYLAHL-----118
77 AGAKIFEPAPGEGNSNSNRKRAVQGPETVTQDCLQIADSETPTIKGSYTFVFWL 136
119 ATLELPQPPQPPVPSVSSGS-----LQALSITDLPTISPSVDL-----157
137 LSFKEGSAALYGOVLYTDITYAMGHLIQRKKVHVFGEDELVLTLPRCINLEBEGDELQAI 196
158 -----SSIFEPVM--SSTWAMQOO-PPRSDHLFGVPSS-----SNMGGGGELQ-AL 199
197 PRE 199
200 ARE 202

RESULT 13
KIRTCB
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C:Accession: B28163; B26408; S00216
R:Ono, Y.; Fujii, T.; Ogita, K.; Kikkawa, U.; Igarashi, K.; Nishizuka, Y.
J. Biol. Chem. 263, 6927-6932, 1988
A:Title: The structure, expression, and properties of additional members of the protein
A:Reference number: A92717; MUID:88198270; PMID:2834397
A:Accession: B28163
A:Molecule type: DNA
A:Residues: 1-737 <ON>
A:Cross-references: GB:M18331; NID:g206182; PIDN:AAA41872.1; PID:g206183
R:Housey, G.M.; O'Brian, C.A.; Johnson, M.D.; Kirschmeier, P.; Weinstein, I.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 1065-1069, 1987
A:Title: Isolation of cDNA clones encoding protein kinase C: evidence for a protein kinase
A:Reference number: A94145; MUID:87147193; PMID:3469647
A:Accession: B26408
A:Molecule type: mRNA
A:Residues: 397-447, 'GORGHLDDREDFGSGAET', 467, 'LSNPTLLLPDQGPPLRQ', 487-545, 'C', 547-636
A:Cross-references: GB:M15523; NID:g206192; PIDN:AAA41877.1; PID:g206193
C:Comment: Protein kinase C epsilon and epsilon' appear to be encoded by the same gene
C:Function:
A:Note: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; pr
C:Keywords: alternative splicing; ATP; autophosphorylation; duplication; phorbol ester B

19 REEMKLEKCVSILPRKESPSVLLSCCLTVVSF-YQVAALQGLDLSRAEL--QGHAEKLP 76
268 RQGLQCKVCKMNVHRCETNAPNC---GVDARGIAKVLADLGVTPDKITNSGQRKKLA 324
77 AGAKIFEPAPGEGNS-SONSKRAVQGP-----EETVTQDC 113
325 AGA---ESFPASGNSPDRSKSAPTSPCDQELKELENNIRKALSTFDNKEHRASSS 381
114 L--QLIADSETPTIKG-----SYTFVFWLSFKRGSALYGOVLYTDITYAMGHLIQ 163

Query Match 7.4%; Score 82.5; DB 1; Length 737;
Best Local Similarity 20.7%; Pred. No. 15;
Matches 50; Conservative 34; Mismatches 88; Indels 69; Gaps 10;

382 TDQIASPGENGEVROGAQKRLGLDFNFIKVLKSGSFGKVMLAELKDEKDEVAV--KVL 439
164 RKKVHVFGEELS-----LVTLPRCINLE-----EGDELQALP 197
440 KQVILQDDVDCTMTKRIILAKRHPYLTQLYCCFQTKDRLFFVMEYVNGGDLMFQIQ 499
198 R 198
500 R 500

RESULT 14
JH0821
95K golgi antigen - human
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
C:Accession: JH0821
R:Fritzler, M.J.; Hamel, J.C.; Ochs, R.L.; Chan, E.K.L.
J. Exp. Med. 178, 49-62, 1993
A:Title: Molecular characterization of two human autoantigens: unique cDNAs encoding 95-
A:Reference number: JH0820; MUID:93301617; PMID:8315394
A:Accession: JH0821
A:Molecule type: mRNA
A:Residues: 1-620 <FRI>
A:Cross-references: EMBL:L06147; NID:g306781; PIDN:AAA35920.1; PID:g306782
A:Experimental source: hepatic carcinoma AT CC HB8065 cell line
A:Note: This protein has alpha-helical structure with absence of beta-sheets

Query Match 7.3%; Score 82; DB 2; Length 620;
Best Local Similarity 25.2%; Pred. No. 14;
Matches 41; Conservative 20; Mismatches 52; Indels 50; Gaps 7;

3 DSTEREQLTSCLKREEMKLEKCVSILPRKESPSVLLSCCLTVVSFYQ--VAALQGLD 60
317 DGLDRE-----EDEDEEEEAQVQPMPSIPEDLESREAVAFNSAVASAESEQ 369
61 ASLRAELQGH-----AEKLPAKAKIFEPAPGEGNSNSNRKRAVQGP---105
370 ARLAGQLKEQVRCCRRLAHLASAKPEAA---APAGTGGDSVCGETHRALQAMEK 425
106 -----EETVTQDCLQIADSETPTIKGSY 130
426 LQSRFMBELMOEKADLKERVELEHRCIQL--SGETDTI--GEY 464

RESULT 15
KIMSCE
protein kinase C (EC 2.7.1.1) epsilon - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 21-Nov-1997
C:Accession: S02270
R:Schaap, D.; Parker, P.J.; Bristol, A.; Kriz, R.; Knopf, J.
FEBS Lett. 243, 351-357, 1989
A:Title: Unique substrate specificity and regulatory properties of PKC-epsilon: a ration
A:Reference number: S02270; MUID:89137541; PMID:2917656
A:Accession: S02270
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-737 <KSC>
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; pr
C:Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid B

F:156-161/Region: pseudophosphorylation motif
F:170-220/Domain: protein kinase C zinc-binding repeat homology <K21>
F:243-292/Domain: protein kinase C zinc-binding repeat homology <K22>
F:406-668/Domain: protein kinase homology <KIN>
F:414-422/Region: protein kinase ATP-binding motif.
F:170,201,204,220/Binding site: zinc (His, Cys, Cys)
F:183,186,209,212/Binding site: zinc (Cys, Cys, His)
F:243,273,276,292/Binding site: zinc (His, Cys, Cys)
F:256,259,281,284/Binding site: zinc (Cys, Cys, His)
F:437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted
F:703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

F:437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted
F:703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

```
Query Match      7.3%; Score 81.5; DB 1; Length 737;
Best Local Similarity 20.7%; Pred. No. 19;
Matches 50; Conservative 33; Mismatches 89; Indels 69; Gaps 10;

QY 19 REEMKLEKCVSILPRKSPVLLSCCLTVVSVFYQVAALQGDLSLRAEL--QGHHAELKP 76
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 268 RQGLQCKVKKNVHRCETNPNC--GVDARGIAKVLADLGVTDPDKITNSGQRRKLA 324
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 77 AGAKIFEPAPCEGNS-SONGRNKRKAVOGP-----EETVTODC 113
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 325 AGA---ESPQASGNSPSEDDRSKAPTSPCDQELKELENNIRKALSFDNRGEHRASSA 381
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 114 L--QLIADSETPTIQG-----SYTFVPWLLSFKEGSALYGVLYTDKTYAMGHLIQ 163
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 382 TDGQLASPGENGVEVRPGQAKRLGLDDEFNFIKVLGKSGFKVMLAELKCKDEVYAV--KVL 439
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 164 RKKVHVFGDELS-----LVTLFRCIQNLE-----EGDELQLAIP 197
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 440 KKDVLQDDDDVDCMTXKRLALARKHPYLTQLYCCFQTKDRLFPVMEYVNGGDLMPQIQ 499
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 198 R 198
   |
Db 500 R 500
```

Search completed: February 3, 2004, 07:45:36
Job time : 16.5644 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:43:37 ; Search time 9.20444 Seconds
(without alignments)
1113.790 Million cell updates/sec

Title: US-09-911-777-1

Perfect score: 1116

Sequence: 1 MDDSTEREQSLTSLCKRE.....ENAIQLDGDVTFFGALKIL 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1042.5	93.4	285	T13B_HUMAN	Q9Y275 homo sapien
2	623.5	55.9	309	T13B_MOUSE	Q9WU72 mus musculus
3	152	13.6	250	TN13_HUMAN	Q75888 homo sapien
4	143	12.8	241	TN13_MOUSE	Q9D777 mus musculus
5	91	8.2	1121	YJ05_YEAST	P47107 saccharomyc
6	88	7.9	664	PRTP_HSVB2	P17587 bovine herp
7	87	7.8	4835	MDN1_GALIA	Q8T5C1 giardia lam
8	84.5	7.6	637	VEL_HPV35	P27220 human papil
9	84	7.5	591	VATA_STRP3	Q8K8T1 streptococc
10	82.5	7.4	228	LB30_ARATH	O81323 arabidopsis
11	82.5	7.4	737	KPC2_RAT	P09216 rattus norv
12	82	7.3	233	TNFA_LAMGL	P59694 lama glama
13	82	7.3	620	GG95_HUMAN	Q08379 homo sapien
14	81.5	7.3	737	KPC2_MOUSE	P16054 mus musculus
15	81.5	7.3	760	CHSX_USTMA	Q99126 ustilago ma
16	80.5	7.2	577	P2B1_DROME	P48456 drosophila
17	80.5	7.2	2314	AKA6_RAT	Q9WVC7 rattus norv
18	80	7.2	233	TNFA_CANFA	P51742 canis famill
19	79	7.1	233	TNFA_TURTR	Q9BEA1 turciops tr
20	78.5	7.0	547	ESTA_DROPS	P25727 drosophila
21	78	7.0	281	COTI_HUMAN	Q9BXJ1 homo sapien
22	78	7.0	473	C1S1_ARATH	P20115 arabidopsis
23	77.5	6.9	356	CMGA_BACSU	P25953 bacillus su
24	77.5	6.9	889	COPP_YEAST	P41811 saccharomyc
25	77.5	6.9	1371	UBR9_HUMAN	Q94966 homo sapien
26	77	6.9	233	TNFA_FELCA	P19101 felis silve
27	77	6.9	431	STE2_YEAST	P06842 saccharomyc
28	76.5	6.9	555	ESTA_DROMI	O16168 drosophila
29	76.5	6.9	561	EST5_RAT	Q63010 rattus norv
30	76.5	6.9	737	KPC2_HUMAN	Q02156 homo sapien
31	76.5	6.9	877	WEE1_SCHPO	P07527 schizosacch
32	76.5	6.9	968	CTDI_HUMAN	O60716 homo sapien
33	76.5	6.9	3214	BPAL_HUMAN	Q03001 homo sapien

34 76 6.8 377 1 KAPR_APLCA P31319 aplysia cal
35 76 6.8 1238 1 B3A2_CAVPO Q920S8 cavia porce
36 75.5 6.8 510 1 Y0BA_BACSU P45917 bacillus su
37 75.5 6.8 531 1 IMA2_CABEL P12776 caenorhabdi
38 75.5 6.8 548 1 ESTA_DROPE O16173 drosophila
39 75 6.7 233 1 TNFA_DELLE Q8WNR1 delphinapce
40 75 6.7 993 1 TSH_DROME P22265 drosophila
41 75 6.7 1042 1 SPA1_HUMAN Q96FS4 homo sapien
42 75 6.7 2436 1 ABC2_HUMAN Q9BZC7 homo sapien
43 74.5 6.7 320 1 PR7R_MMTVG P10261 mouse mamma
44 74.5 6.7 324 1 PR7L_MMTVG P03321 mouse mamma
45 74.5 6.7 435 1 YSOI_CABEL Q10127 caenorhabdi

ALIGNMENTS

RESULT 1
T13B_HUMAN
ID T13B_HUMAN STANDARD; PRT; 285 AA.
AC Q9Y275;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 13B (TNF and APOL-
DE related leukocyte expressed ligand 1) (TALL-1) (B lymphocyte
DE stimulator) (BLYS) (B cell-activating factor) (BAFF) (Dendritic cell-
DE derived TNF-like molecule).
GN TNFSF13B OR TALL1 OR BLYS OR BAFF OR ZTNF4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RX MEDLINE=99260341; PubMed=10331498;
RA Shu H.-B., Hu W.-H., Johnson H.;
RT "TALL-1 is a novel member of the TNF family that is down-regulated by
RT mitogens";
RL J. Leukoc. Biol. 65:680-683(1999).
RN [2]
SEQUENCE FROM N.A., AND SEQUENCE OF 134-148.
RX MEDLINE=99288033; PubMed=10359578;
RA Schneider P., Mackay F., Steiner V., Hofmann K., Bodmer J.-L.,
RA Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,
RA Valmori D., Romero P., Werner-Pavre C., Zubler R.H., Browning J.L.,
RA Tschoopp J.;
RT "BAFF, a novel ligand of the tumor necrosis factor family, stimulates
RT B cell growth";
RL J. Exp. Med. 189:1747-1756(1999).
RN [3]
SEQUENCE FROM N.A.
RC TISSUE=Monocytes, and Neutrophils;
RX MEDLINE=99329343; PubMed=10398604;
RA Moore P.A., Belvedere O., Orr A., Pieri K., LaFleur D.W., Feng P.,
RA Soppet D., Charters M., Gentz R., Pamerlee D., Li Y., Galperina O.,
RA Giri J., Roschke V., Nardelli B., Carrell J., Sosnovtseva S.,
RA Greenfield W., Ruben S.M., Olsen H.S., Fikes J., Hilbert D.M.;
RT "Blyis: member of the tumor necrosis factor family and B lymphocyte
RT stimulator";
RL Science 285:260-263(1999).
RN [4]
SEQUENCE FROM N.A.
RA Farrah T., Gross J., Piddington C., O'Hara P.;
RT "Homo sapiens homolog of tumor necrosis factor";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
SEQUENCE FROM N.A.
RC TISSUE=Dendritic cell;
RA Zhang W., Wan T., Yu Y., Cao X.;
RT "A novel dendritic cell-derived TNF-like molecule";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [6]

RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Ziegler B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny E.J., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [7]
RP SEQUENCE OF 1-135 FROM N.A., AND VARIANT THR-105.
RA Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
RT "New polymorphisms of human BLYS gene.";
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
RN [8]
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Thell L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity.";
RL Nat. Immunol. 1:252-256 (2000).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 142-285.
RX MEDLINE=21842897; PubMed=1853672;
RA Liu Y., Xu L., Opalka N., Kappler J., Shu H.-B., Zhang G.;
RT "Crystal structure of STALL-1 reveals a virus-like assembly of TNF
RT family ligands.";
RL Cell 108:383-394 (2002).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 136-285.
RX MEDLINE=21686304; PubMed=11827482;
RA Karpusas M., Cachero T.G., Qian F., Boriack-Sjodin A., Mullen C.,
RA Strauch K., Hsu Y.-M., Kalled S.L.;
RT "Crystal structure of extracellular human BAFF, a TNF family member
RT that stimulates B lymphocytes.";
RL J. Mol. Biol. 315:1145-1154 (2002).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 134-285.
RX MEDLINE=21912420; PubMed=11862220;
RA Oren D.A., Li Y., Volovik Y., Morris T.S., Dharja C., Das K.,
RA Galperina O., Gentz P., Arnold E.; recognition.";
RT "Structural basis of BlyS receptor recognition.";
RL Nat. Struct. Biol. 9:288-292 (2002).
CC -!- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and TNFRSF17/BCMA.
CC TNFSF13/APRIL binds to the same 2 receptors. Together, they form a
CC 2 ligands -2 receptors pathway involved in the stimulation of B-
CC and T-cell function and the regulation of humoral immunity. A
CC third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the
CC survival of mature B-cells and the B-cell response.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN PERIPHERAL BLOOD
CC LEUKOCYTES AND IS SPECIFICALLY EXPRESSED IN MONOCYTES AND
CC MACROPHAGES. ALSO FOUND IN THE SPLEEN, LYMPH NODE, BONE MARROW, T-
CC CELLS AND DENDRITIC CELLS. A LOWER EXPRESSION SEEN IN PLACENTA,
CC HEART, LUNG, FETAL LIVER, THYMUS, AND PANCREAS.

CC -!- INDUCTION: UPREGULATED BY EXPOSURE TO INTERFERON-GAMMA. DOWN-
CC REGULATED BY PHORBOL MYRISTATE ACETATE/IONOMYCIN TREATMENT.
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -!- PTM: N-glycosylated.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF136293; AAD29421.1; -;
CC EMBL; AF116456; AAD25356.1; -;
CC EMBL; AF132600; AAD21092.1; -;
CC EMBL; AF186114; AAF01432.1; -;
CC EMBL; AF134715; AAF60219.1; -;
CC EMBL; AB073225; BAB90856.1; -;
CC EMBL; BC020674; AAH20674.1; -;
CC PDB; 1XXG; 03-APR-02.
CC PDB; 1XD7; 12-NOV-02.
CC PDB; 1JH5; 08-FEB-02.
CC Genew; HGNC:11929; TNFSF13B.
CC MIM; 603969; -;
CC GO; GO:0005625; C:soluble fraction; TAS.
CC GO; GO:0008283; P:cell proliferation; TAS.
CC GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR006052; TNF_family.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; FALSE NEG.
CC PROSITE; PS50049; TNF_2; 1.
CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure;
CC Polymorphism.
CC CHAIN 1 285 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
CC CHAIN 134 285 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
CC DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 47 67 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC (POTENTIAL).
CC DOMAIN 68 285 EXTRACELLULAR (POTENTIAL).
CC SITE 133 134 CLEAVAGE.
CC DISULFID 232 245
CC CARBOHYD 124 124
CC CARBOHYD 242 242
CC VARIANT 105 105
CC STRAND 146 151
CC TURN 153 154
CC STRAND 158 160
CC TURN 161 162
CC STRAND 163 165
CC STRAND 168 174
CC TURN 178 181
CC TURN 182 183
CC STRAND 184 187
CC STRAND 191 201
CC STRAND 208 215
CC TURN 221 222
CC STRAND 226 234
CC STRAND 243 253
CC TURN 255 256
CC STRAND 258 263
CC TURN 266 267
CC STRAND 270 270
CC TURN 274 276
CC STRAND 278 283
CC SEQUENCE 285 AA; 31222 MW; 48ED0D7AB38C8867 CRC64;

Query Match 93.4%; Score 1042.5; DB 1; Length 285;
Best Local Similarity 76.5%; Pred. No. 2.9e-90;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTERQSLTSCIKKEEMKKECVSILPKESPSV-----LLSCC 44
DB 1 MDDSTERQSLTSCIKKEEMKKECVSILPKESPSV-----LLSCC 60

QY 45 LTVVSFYQVAALQGLDLSLRAELQGHAEKLPAGA-----KIFEPAP 87
DB 61 LTVVSFYQVAALQGLDLSLRAELQGHAEKLPAGA-----KIFEPAP 120

QY 88 GEGNSSQNRKRAVQGPETVTQCLQIADSETPTIQKGYTFVWLLSPKRGSL-- 145
DB 121 GEGNSSQNRKRAVQGPETVTQCLQIADSETPTIQKGYTFVWLLSPKRGSL-- 180

QY 146 -----YGVLYTDKTYANGHLIQRKVVHVGDELSTLFRQION----- 185
DB 181 KENKILVKETGYFFTYGVLYTDKTYANGHLIQRKVVHVGDELSTLFRQIONPPTL 240

QY 186 -----LEEGDELQLAIPRENAQISLDGVTFFGALKLL 218
DB 241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGVTFFGALKLL 285

RESULT 2
ID T13B MOUSE STANDARD; PRT; 309 AA.
AC Q9WU72.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 13B (B cell-activating factor) (BAFF).
GN TNFSF13B OR BAFF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] SEQUENCE FROM N.A.
RP MEDLINE=99288033; PubMed=10359578;
RA Schneider P., Mackay F., Steiner V., Hofmann K., Bodmer J.-L.,
RA Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,
RA Valmori D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L.,
RA Tschopp J.;
RT "BAFF, a novel ligand of the tumor necrosis factor family, stimulates B cell growth.";
RL J. Exp. Med. 189:1747-1756(1999).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT SER-79.
RC STRAIN=NZB.
RX MEDLINE=21850530; PubMed=11862414;
RA Jiang Y., Ohtsui M., Abe M., Li N., Xiu Y., Wen X.S., Shirai T.,
RA Hirose S.;
RT "Polymorphism and chromosomal mapping of the mouse gene for B-cell activating factor belonging to the tumor necrosis factor family (Baff) and association with the autoimmune phenotype.";
RL Immunogenetics 53:810-813(2001).
CC -!- FUNCTION: Cytokine that binds to TNFSF13B/TACI and TNFSF17/BCMA. TNFSF13/APRIL binds to the same 2 receptors. Together, they form a 2 ligands -2 receptors pathway involved in the stimulation of B- and T-cell function and the regulation of humoral immunity. A third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the survival of mature B-cells and the B-cell response.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF119383; AAD22475.1; -
DR EMBL; AF352245; AAL83939.1; -
DR MGI; MGI:1344376; Tnfsl3b.
DR InterPro; IPR006052; TNF_family.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE NEG.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor;
KW Polymorphism.
FT CHAIN 1 309 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT CHAIN 127 309 MEMBER 13B, MEMBRANE FORM.
FT CHAIN 127 309 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT DOMAIN 1 47 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 48 68 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 69 309 (POTENTIAL).
FT SITE 126 127 EXTRACELLULAR (POTENTIAL).
FT DISULFID 256 269 CLEAVAGE (BY SIMILARITY).
FT CARBOHYD 117 117 BY SIMILARITY.
FT CARBOHYD 266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 79 79 N -> S (IN STRAIN NZB).
SQ SEQUENCE 309 AA; 34192 MW; F3DE6056E66034B4 CRC64;

Query Match 55.9%; Score 623.5; DB 1; Length 309;
Best Local Similarity 47.4%; Pred. No. 5.5e-51;
Matches 147; Conservative 24; Mismatches 46; Indels 93; Gaps 7;

QY 1 MDDSTER-EQSLTSCIKKEEMKKECVSILPKESPS-----VLLS 42
DB 1 MDESAKTLPPCLCFCSEKGEKMKV-GYDPTTPOKEGAWFGICRDGRLLAATLLALLS 59

QY 43 CCLTVSPYQVAALQGLDLSLRAELQGH-----AEKLPAGAKFEPPAGEGNS 93
DB 60 SSTFTMSLYQALQADLMNLMELQSYRGSAATPAAGAPELTAGVKULTTAAAPPHNS 119

QY 94 QNSNRKRAVQGPET-----VTQDCQLIADSET 122
DB 120 RGHNRRAFGQPEETEQQVDLSAPPCLPCGRHSQHDNGMNLNIIQDCQLIADSDT 179

QY 123 PTIQKGYTFVWLLSPKRGSL-----YGVLYTDKTYANGHLIQRK 165
DB 180 PTIRKGTFTVPVWLLSPKRGSL-----YGVLYTDKTYANGHLIQRK 239

QY 166 KVHVFGDELSLVTLFRQION-----LEEGDELQLAIPRENAQISLDG 208
DB 240 KVHVFGDELSLVTLFRQIONMPTLPNNSCYSAGIARLEEGDELQLAIPRENAQIS 299

QY 209 VTFFGALKLL 218
DB 300 DTFFGALKLL 309

RESULT 3
ID TN13 HUMAN STANDARD; PRT; 250 AA.
AC O75888; Q96HV6; Q9PIM8; Q9PIM9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 43, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 13 (A proliferation-inducing ligand) (APRIL) (TNF-and APOL-related leukocyte expressed ligand 2) (TALL-2) (TNF-related death ligand-1) (TRDL-1).
GN TNFSF13 OR APRIL OR TALL2 OR ZTNF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Db 85 EQSDALEAWENGERSRKRRAVLTKQKKQKSHLVHLVLPINAT-SKDDSDVTEVMWQPALR 143
Qy 141 RGSA-----LYGOVLYTDKTYAMGHILQKVVHFGDELSTLFRCI 183
Db 144 RRGGLQAQGYGVRIQDAGVLYLSQVLFQDVTFTMGQVVSRE-----GQGRQETLFRCI 197
Qy 184 Q-----NLEEGDELQALAIAPRENAQISLDGVDVTFPGALKL 217
Db 198 RSMSPHPRAYNCYSAGVFLHQGDLISVLIIPARAKNLSPHGTFLGFKVL 250

RESULT 4
TN13 MOUSE
ID TN13 MOUSE STANDARD; PRT; 241 AA.
AC Q9D777; Q9ERP1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 13 (A proliferation-inducing ligand) (APRIL).
GN TNFSF13 OR APRIL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=21170294; PubMed=10973284;
RY Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc H., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RA "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating humoral immunity";
RT Nat. Immunol. 1:252-256(2000).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RY Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J., Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S., Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
RL
CC -!- FUNCTION: Cytokine that binds to TNFSF13B/TACI and to TNFSF17/BCMA. May be implicated in the regulation of tumor cell growth. May be involved in monocyte/macrophage-mediated immunological processes.
CC -!- SUBUNIT: Homotrimer (Potential).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by proteolytic processing.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
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CC -----
CC EMBL; AF294825; AAC22534.1; --
CC EMBL; AK009514; BAB26332.1; --
CC MGD; MGI:1916833; Tnfrsf13.
CC GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
CC InterPro; IPR006052; TNF_family.
CC Pfam; PF00229; TNF; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Immune response; Glycoprotein.
FT PROPEP 1 95
FT CHAIN 96 241
FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT MEMBER 13.
FT CLEAVAGE (BY URIN) (BY SIMILARITY).
FT DISULFID 187 202
FT CARBOHYD 115 115
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 120 120
FT MISSING (IN REF. 2).
SQ SEQUENCE 241 AA; 26889 MW; 4B96D03BDBC712A4 CRC64;
Query Match 12.8%; Score 143; DB 1; Length 241;
Best Local Similarity 26.3%; Pred. No. 3.8e-06;
Matches 56; Conservative 23; Mismatches 68; Indels 66; Gaps 7;
Qy 57 QGDLASIRAE---LQGHHAELKLPAGAKIFE-----PPAPGEGNSSQNRKNRAVOGPEE 107
Db 43 QTELQSLREVRSLQSGSGPSQKQGERPQSLWQSQSPDLBAWKDGAKRRRAVLTKGH 102
Qy 108 TVTQDCLQI-----ADSETPTQKSGYTFVPWLLSFKRGSA----- 144
Db 103 KKHSVLHLVPVNTSKADSV-----TEVMQPVLRGRGLEAQGDIVRVWDGTGY 154
Qy 145 -LYGOVLYTDKTYAMGHILQKVVHFGDELSTLFRCIQ----- 184
Db 155 LLYSQVLFHDVTFMTMGQVVSRE-----GQGRRETLPFCIRSPDPDRAYNCYSAGVF 208
Qy 185 NLEEGDELQALAIAPRENAQISLDGVDVTFPGALKL 217
Db 209 HLHQGDIIITVKIPRANAKLSLSPHGTFLGFKVL 241

RESULT 5
YJ09 YEAST
ID YJ09 YEAST STANDARD; PRT; 1121 AA.
AC P47107;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Hypothetical 127.4 kDa protein in HUL4-GEF1 intergenic region.
GN YJ039W OR J1614.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang M.-E., Chua J.-C., Galibert F.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; Z49538; CAA89566.1; --
CC PIR; S57058; S57058.
CC SGD; S0003800; YJ039W.

RESULT 7

SQ SEQUENCE 591 AA; 64982 MW; 296ACDC372009340 CRC64;
 Query Match 7.5%; Score 84; DB 1; Length 591;
 Best Local Similarity 22.0%; Pred. No. 4;
 Matches 54; Conservative 30; Mismatches 71; Indels 90; Gaps 12;
 QY 1 MDDSTERSQRLTSCCKREEMKLEKCVSILPRKES-PSVLLSCCLTVVSYQVAAA----- 55
 DB 328 MADSTSRWAEALREMSGLQEM-----PGDEGYPAYLGS---RAEYERAGRVRT 375
 QY 56 -----LQGDLASRLAEQGHAEKLPAGAKIFEPAPGEGNSQNSRKNRAVQGPFEFTV 110
 DB 376 LGSQERECTITAIGA-----VSPPGCDISEP-----VT 403
 QY 111 QDCQLQIA-----DSEPTTKGSYTFVPWLLSFKSGSALYGQVLYTDKTYAMGHILQK- 166
 DB 404 QNTLRIIKVFWGLDAPLQRRHFPAINLWTSYS-----LYQDD---VGSYIDRKQE 451
 QY 167 -----VHVFGDELSLVTLPFCI--QNLEEGDELQLAIPR-----ENALSLD 206
 DB 452 SNWSNKVTRMAILLOREASLEIVLVGLDSLSEQDLTMVARQIREYDLYQNAFDSVD 511
 QY 207 GDVTF 211
 DB 512 TFTSF 516
 RESULT 10
 ID LB30 ARATH STANDARD; PRT; 228 AA.
 AC 081323;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE LOB domain protein 30.
 GN LB30 OR AT4G00220 OR FGN15.4.
 OS Arabidopsis thaliana (Mouse ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22063719; PubMed=12068116;
 RA Shuai B., Reynaga-Pena C.G., Springer P.S.;
 RT "The LATERAL ORGAN BOUNDARIES Gene defines a novel, plant-specific
 RL gene family."
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
 RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Maché R., Mueller M.,
 RA Kreis M., Delzeny M., Puigdomenech P., Watson M., Schmidheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridler P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
 RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 RA De Keyser A., Buyssehaert C., Gielens J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., Mclay K., Mayes R.,
 RA Pettett A., Rajandream M.A., Lyne M., Benes V., Reckmann S.,
 RA Borkova D., Bloeker H., Schaefer M., Grimm M., Loehnert T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Argirion A., Vitale D., Liguori R., Piravandi E.,
 RA Masseret O., Quigley P., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lechary A., Aubourg S.,
 RA Chedford F., Cooke R., Berger C., Monfort M., Bagues M., Terol J., Torres A.,
 RA Gibbons T., Weber N., Vandenbol M., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Perez-Perez A., Purnelle B., Heber S., Heber S., Francis P., Bielek C.,
 RA Heijnen L., Schwarz S., Scholler P., Mewes H.-W., Stocker S.,
 RA Friseman D., Haase D., Lencke K., Wilson R.K., de la Bastide M., Habermann K.,
 RA Zaccaria P., Bevan M., Nelson R.K., Schutz K., Huang E., Spiegel L.,
 RA Parnell L., Dedhia N., Gnoj L., Sheet P., Cordes M., Abu-Threiden J.,
 RA Sekhon M., Murray J., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Stoneking T., Kallik J., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Lattelle P., Courtney L., Miller N., Greco T., Kemp K., Hillier L.,
 RA Minx P., Bentley D., Fulton B., Mardis E., Dante M., Pepin K., Hillier L.,
 RA Kramer J., Fulton L., Mardis E., Andrews S., Geisel C., Layman D.,
 RA Nelson J., Spiech J., Ryan E., Jones K., Drone K., Cotton M., Joshi C.,
 RA Du H., Ali J., Berghoff A., Strong C., Sun H., Lamar B., Yordan C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
 RA Seaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Granat S., Shohdy N., Hasegawa A., Hamed A., Lodhi M., Johnson A.,
 RA Chen E., Marra M., Martienssen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 RT thaliana."
 RL Nature 402:769-777(1999).
 CC -1- TISSUE SPECIFICITY: Expressed in roots, stems, leaves and flowers.
 CC -1- SIMILARITY: Contains 1 LOB domain.
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 CC -----
 DR EMBL; AF432232; AAL27613.1; -
 DR EMBL; AF069299; AAC19300.1; -
 DR EMBL; AL461471; CAB80780.1; -
 DR FIR; T01350; T01350.
 DR InterPro; IPR004883; DUF260.
 DR Pfam; PF03195; DUF260; 1.
 DR PROSITE; PS50891; LOB; 1.
 FT DOMAIN 16 118
 SQ SEQUENCE 228 AA; 23968 MW; CAE3F2DA4C78A209 CRC64;
 Query Match 7.4%; Score 82.5; DB 1; Length 228;
 Best Local Similarity 25.1%; Pred. No. 1.6;
 Matches 46; Conservative 23; Mismatches 63; Indels 51; Gaps 9;
 QY 18 KREEMKLEKCVSILPRKESPSVLLSCCLTVVSYF-YQVAAQGLASRLAEQGHAEKLP 76
 DB 70 KRPAVVSICFEAQARLRDP--IYGVSHVSLQVQVVSQVLSQVLSYLAHL----- 118
 QY 77 AGAKIFPPAPGEGNSQNSRKNRAVQGPFEFTVQDCQLQIADSETPTIQKGSYTFVFWL 136
 DB 119 ATLEPQPPQVPSVSGS-----LQALSIDLPTISVVDL----- 157
 QY 137 LSPKRGSLYQGVLYTDKTYAMGHILQKQVHVFGDELSTVLPFCIONLEEGDELQAI 196
 DB 158 -----SSIEPEVNV--SSTWAMQQQ-PRPSDHLFGVPSS-----SNMGGGGELQ-AL 199
 QY 197 PRE 199
 DB 200 ARE 202
 RESULT 11
 KPCE_RAT
 ID KPCE_RAT
 AC P09216;
 DT 01-MAR-1989 (Rel. 10, Created) PRT; 737 AA.

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CC EMBL; AB107646; BAC75383.1; -
CC PROSITE; PS00251; TNF 1; 1.
CC PROSITE; PS0049; TNF 2; 1.
CC Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
CC CHAIN 1 233
FT CHAIN 77 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM (BY
FT FT SIMILARITY).
FT FT TUMOR NECROSIS FACTOR, SOLUBLE FORM (BY
FT FT SIMILARITY).
FT FT CYTOLASMIC (POTENTIAL).
FT FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (BY SIMILARITY).
FT FT EXTRACELLULAR (POTENTIAL).
FT FT PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT FT CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT FT BY SIMILARITY.
FT FT DISULFID 145 177
FT SEQUENCE 233 AA; 25437 MW; F5C07837505FBD86 CRC64;

Query Match 7.3%; Score 82; DB 1; Length 233;
Best Local Similarity 22.5%; Pred. No. 1.9;
Matches 52; Conservative 29; Mismatches 92; Indels 58; Gaps 9;
QY 31 LPKBE-SPSVLLSC-CLTVSVFYVAALQGDLSLRAELQGHAKLPAGAKIPEPPAPG 88
DB 17 LPKAGGQGGRRCLSLFLLVAGATTFLCLHFGVIGPQKELLTGQIWNPLAQT 76
QY 89 EGNSSQNRKRAVQGPETVTQDCLQ-----LIA-----DSEPTTIQKGSYTFVP 134
DB 77 LRSSQASRDXVAVHVPAAQQLQWEKRPANLLANGVKLEDNQLVVPDGLY---- 132
QY 135 WLLSPKRSALYGVLYTDK-----TYANGHLIQKVVHFGDELSVTLFR--C----- 182
DB 133 -----LIYSQVLFSGQRCFSTFVLTHITISLAVS-YPNKANLLSAIKSPCQGGTS 182
QY 183 -----IQNLEBGEDELQAIIPRENAQISLDGVDVTFPGALKL 217
DB 183 EBAEAKPWYPIYLGQVLEKDDRLSAEINPNVLDFAESGVVFGIAL 233

RESULT 13
GG95_HUMAN
ID GG95_HUMAN STANDARD; PRT; 620 AA.
AC Q08379;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Golgin-95.
GN GOLGA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93301617; PubMed=8315394;
RA Fritzler M.J., Hamel J.C., Ochs R.L., Chan E.K.L.;
RT "Molecular characterization of two human autoantigens; unique cDNAs
RT encoding 95- and 160-kD proteins of a putative family in the Golgi
RT complex.";
RL J. Exp. Med. 178:49-62(1993).
CC -!- FUNCTION: GOLGI AUTOANTIGEN; MAY HAVE A FUNCTION IN THE
CC PROCESSING AND TRANSPORT OF PROTEINS THROUGH THE GOLGI.
CC -!- DOMAIN: EXTENDED ROD-LIKE PROTEIN WITH COILED-COIL DOMAINS.
CC -!- SIMILARITY: HIGH, TO RAT CIS-GOLGI MATRIX PROTEIN GML30.
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CC EMBL; L06147; AAA3920.1; -
CC PIR; JH0821; JH0821.
CC Genew; HGNC:4425; GOLGA2.
CC MIM; 602580; -
CC GO; GO:0005794; C:Golgi apparatus; TAS.
KW Golgi stack; Coiled coil.
FT DOMAIN 5 336 COILED COIL (POTENTIAL).
FT DOMAIN 352 510 COILED COIL (POTENTIAL).
FT DOMAIN 67 73 POLY-GLU.
FT DOMAIN 322 333 POLY-GLU.
FT SEQUENCE 620 AA; 70472 MW; 54B31A0FBB42BFC8 CRC64;

Query Match 7.3%; Score 82; DB 1; Length 620;
Best Local Similarity 25.2%; Pred. No. 6.6;
Matches 41; Conservative 20; Mismatches 52; Indels 50; Gaps 7;
QY 3 DSTEREQSLTSCCLKKEEMKKECVSILPKESPSVLLSCCLTVWSFYQ--VAALQDGL 60
DB 317 DGLDRB-----EEDDEEEEAVALPQPMPSIPEDLESREANVAFFNSAVASAEQ 369
QY 61 ASLRAELQGH-----AEKLPAGAKIPEPPAPGEGNSSQNRKRAVQGP--- 105
DB 370 ARLGQLKEQVRCRRRLAHLASAKPEAA---APAGTGGDSVCGETHRALQAMEK 425
QY 106 -----EETVQDCLQIADSETPIQKSY 130
DB 426 LQSRFMELOEKADLKERVELEHRCIQL--SGETDTI--GEY 464

RESULT 14
KPCE_MOUSE
ID KPCE_MOUSE STANDARD; PRT; 737 AA.
AC P16054;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
GN PKCE OR PKCE OR PKCEA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89137541; PubMed=2917656;
RA Schaap D., Parker P.J., Bristol A., Kriz R., Knopf J.;
RT "Unique substrate specificity and regulatory properties of
RT PKC-epsilon: a rationale for diversity.";
RL FEBS Lett. 243:351-357(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98127436; PubMed=9467942;
RA Wang Q.J., Acs P., Goodnight J., Blumberg P.M., Mischak H.,
RA Mushinski J.F.;
RT "The catalytic domain of PKC-epsilon, in reciprocal PKC-delta and -
RT epsilon chimeras, is responsible for conferring tumorigenicity to
RT NIH3T3 cells, whereas both regulatory and catalytic domains of
RT PKC-epsilon contribute to in vitro transformation.";
RL Oncogene 16:53-60(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Wheeler D.L.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN

CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -|- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -|- SIMILARITY: Contains 1 C2 domain.
CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF028009; AAB84189.1; --
CC EMBL; AF325507; AAG53692.1; --
CC PIR; S02270; KIMSCE.
CC HSSP; P28867; IPTQ.
CC MGD; MGI:97599; Pkckc.
CC GO; GO:0004699; P.calcium independent protein kinase C activity; IDA.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002219; DAG_PE-bind.
CC InterPro; IPR000961; Pkinase C.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00168; C2; 1.
CC Pfam; PF00130; DAG_PE-bind; 2.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00433; pkinase C; 1.
CC PRINTS; PRO00008; DAGPEDOMAIN.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00109; C1; 2.
CC SMART; SM00239; C2; 1.
CC SMART; SM00133; S_TK_X; 1.
CC SMART; SM00220; S_TK; 1.
CC PROSITE; PS50004; C2 DOMAIN 2; 1.
CC PROSITE; PS00479; DAG PE BIND DOM 1; 2.
CC PROSITE; PS50081; DAG PE BIND DOM 2; 2.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS50011; PROTEIN KINASE DOM; 1.
CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC Repeat; ATP-binding; Transferase; Phosphorylation;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT DOMAIN 1 99 C2 DOMAIN.
FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 408 668 PROTEIN KINASE.
FT NP_BIND 414 422 ATP (BY SIMILARITY).
FT BINDING 437 437 ATP (BY SIMILARITY).
FT ACT_SITE 532 532 BY SIMILARITY.
FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 710 710 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 737 AA; 83560 MW; 7AEBB8CC10C99F57 CRC64;
Query Match 7.3%; Score 81.5; DB 1; Length 737;
Best Local Similarity 20.7%; Pred. No. 9.1;
Matches 50; Conservative 33; Mismatches 89; Indels 69; Gaps 10;
QY 19 REEMKLEKCVSLIPKSPSVLLSCCLTVVSVYQVAALQGLDASLRAEL--QGHAELKIP 76
Db 268 RQGLQCKVKCMNVHRCETNAPNC---GVDARGIAKVLADLGVTDPKITNSGQRKKLA 324
QY 77 AGAKIFPEPPAPEGNS--SNSNRKRAVQCP-----EETVQDC 113
Db 325 AGA---ESPQASGNSPSDDRSKAPTSPCDQLKELENNIRKALSFDNRGEEHRASSA 381
QY 114 L--QLIADSETTIQKG-----SYTFVPWLLSFKRGSALYGVLYTDKTYAMGHLIQ 163
Db 382 TDGQLASPGENGVEVRPGQAKRLGLDDEFNFIKVLKSGSGKVMIAELKKGDEYAV--KVL 439
QY 164 RKKVHVFGDLS-----LVTLFRCIQNL-----EGDELQALP 197

Db 440 KKDVLQDDVDCTMTKRIILALARKHYLTQLYCCFQTKDRLFFVMEYVNGDLMFQIQ 499
QY 198 R 198
Db 500 R 500
RESULT 15
CHSX_USTMA STANDARD; PRT; 760 AA.
ID CHSX_USTMA Q99126;
AC 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Chitin synthase 1 (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl
DE transferase 1).
GN CHS1.
OS Ustilago maydis (Smut fungus).
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=5270;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RK32 / A2B3;
RX MEDLINE=97086517; PubMed=8932711;
RA Xoonoatle-Cazares B., Leon-Ramirez C., Ruiz-Herrera J.;
RT "Two chitin synthase genes from Ustilago maydis";
RL Microbiology 142:377-387(1996).
CC -|- FUNCTION: PLAYS A MAJOR ROLE IN CELL WALL BIOGENESIS.
CC -|- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + (1,4)-(N-acetyl-
CC beta-D-glucosaminyl) (N) = UDP + (1,4)-(N-acetyl-beta-D-
CC glucosaminyl) (N+1).
CC -|- SUBCELLULAR LOCATION: Plasma membrane-bound.
CC -|- SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X87748; CAB61027.1; --
CC PIR; S55520; S55520.
CC InterPro; IPR004834; Chitin synth.
CC Pfam; PF01644; Chitin synth; 1.
CC ProDom; PD002998; Chitin synth; 1.
KW Transferase; Glycosyltransferase; Transmembrane; Cell wall;
KW Multigene family.
SQ SEQUENCE 760 AA; 85181 MW; 9377000F57410993 CRC64;
Query Match 7.3%; Score 81.5; DB 1; Length 760;
Best Local Similarity 21.1%; Pred. No. 9.5;
Matches 39; Conservative 33; Mismatches 58; Indels 55; Gaps 8;
QY 85 PAPEGNSQNSNRKRAVQ-----GPEETVQDCQLIADSETTIQKSYTFVPWL 136
Db 226 PAPERGAQRHRTKCNVRLTKKPHSGLPVTKLTQTLFTRAEDEFTTMRYSAVTCDDPTD 285
QY 137 L--SPKRGSAALYGO-----VLYTD-----KTY-----AMGHLIQRKKVHVFGDE-- 173
Db 286 LERFETLPALYGRHTELFIAITWNEDEVLCFTFHGVMKNIAHLCSNRKSRTWKGGDW 345
QY 174 ----LSLVT-----LFRCI-----ONLEGEDELQALIPRENAQISLDGVD 209
Db 346 KKVVAIISDCRKKIHPRVLDCLAAIGVYQGVAKNMWYDGKVRHAHLYEYTTQLSIDSNL 405
QY 210 TFFGA 214
Db 406 QFKGA 410

Search completed: February 3, 2004, 07:44:14
Job time : 12.2044 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:43:37 ; Search time 29.0667 Seconds
(without alignments)
1935.395 Million cell updates/sec

Title: US-09-911-777-1
Perfect score: 1116
Sequence: 1 MDDSTERQSLTSLCKRE.....ENAIQLSDGDVTFGALKLL 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23.:

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	750.5	67.2	208	Q8IZI6	Q8IZI6 homo sapien
2	677	60.7	174	Q8IZI5	Q8IZI5 homo sapien
3	610	54.7	258	Q8BZM8	Q8BZM8 mus musculus
4	596	53.4	158	Q8IZI4	Q8IZI4 homo sapien
5	497.5	44.6	288	Q8JHJ4	Q8JHJ4 gallus gall
6	252.5	22.6	199	Q8BWP2	Q8BWP2 mus musculus
7	249.5	22.4	194	Q8BVA3	Q8BVA3 mus musculus
8	152	13.6	250	Q8NFH7	Q8NFH7 homo sapien
9	146	13.1	410	Q8BX32	Q8BX32 mus musculus
10	140.5	12.6	330	Q8IZK7	Q8IZK7 homo sapien
11	91.5	8.2	267	Q8B67	Q8B67 rhizobium 1
12	91.5	8.2	695	Q8W2R3	Q8W2R3 oryza sativ
13	88	7.9	1746	Q8AXN0	Q8AXN0 glaucosphae
14	87.5	7.8	240	Q85896	Q85896 synecocyst
15	87.5	7.8	748	Q8W0N1	Q8W0N1 oryza sativ
16	87.5	7.8	1524	Q8RYN2	Q8RYN2 oryza sativ

17	86.5	7.8	3551	11	Q99BS4	Q99BS4 mus musculus
18	86.5	7.8	3576	11	Q9QZM2	Q9QZM2 mus musculus
19	85	7.6	213	16	Q9JUY1	Q9JUY1 neisseria m
20	85	7.6	475	6	Q8WXX8	Q8WXX8 bos taurus
21	85	7.6	475	11	Q8VHF9	Q8VHF9 rattus norv
22	84.5	7.6	325	15	Q90188	Q90188 mouse mamma
23	84.5	7.6	388	16	Q8R9D3	Q8R9D3 thermococ
24	84.5	7.6	1653	5	Q9VSM1	Q9VSM1 drosophila
25	84.5	7.6	1709	5	Q9VSM0	Q9VSM0 drosophila
26	84.5	7.6	2136	4	Q8NFU7	Q8NFU7 homo sapien
27	84	7.5	563	16	Q9S119	Q9S119 streptococ
28	84	7.5	563	16	Q8DQW7	Q8DQW7 streptococ
29	84	7.5	573	16	Q8KBT1	Q8KBT1 streptococ
30	83.5	7.5	360	16	Q25195	Q25195 helicobacte
31	83.5	7.5	596	10	Q9C977	Q9C977 arabidopsis
32	83.5	7.5	693	10	Q94H08	Q94H08 oryza sativ
33	83	7.4	213	16	Q9JZW7	Q9JZW7 neisseria m
34	83	7.4	384	2	Q9F7E6	Q9F7E6 acinetobact
35	83	7.4	591	16	Q9AIQ3	Q9AIQ3 streptococ
36	83	7.4	694	3	Q8TFL0	Q8TFL0 candida gla
37	83	7.4	809	11	Q8CDE6	Q8CDE6 mus musculu
38	82	7.3	990	4	Q9NYF9	Q9NYF9 homo sapien
39	82	7.3	1584	5	Q8WQ43	Q8WQ43 leishmania
40	81.5	7.3	315	15	Q9WHV8	Q9WHV8 mouse mamma
41	81.5	7.3	325	15	Q9WHV9	Q9WHV9 mouse mamma
42	81	7.3	177	10	Q9MS11	Q9MS11 oryza sativ
43	81	7.3	315	15	Q83411	Q83411 mouse mamma
44	81	7.3	315	15	Q83400	Q83400 mouse mamma
45	81	7.3	458	3	Q9UV75	Q9UV75 glomus intr

ALIGNMENTS

RESULT 1

Q8IZI6 PRELIMINARY; PRT; 208 AA.
ID Q8IZI6
AC Q8IZI6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE B-lymphocyte stimulator (Fragment).
GN TNFSF13B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RL Gao H., He F., Li R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY129226; AAN08422.1; -.
FT NON_TER
SQ SEQUENCE 208 AA; 22767 MW; EEA31D227033AA53 CRC64;

Query Match	67.2%	Score 750.5;	DB 4;	Length 208;
Best Local Similarity	75.0%;	Pred. No. 6e-69;		
Matches 156;	Conservative 0;	Mismatches 1;	Indels 51;	Gaps 3;
QY	62	SLRAELQGHAEKLPAGA-----	KIPEPPAPGEGNSQNSRNKRAVQG	104
Db	1	SLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFPEPPAPGEGNSQNSRNKRAVQG	60	
QY	105	PEETVTQDCLQIADSETPTIOKGSYTFVPWLLSFKGSGAL-----	YG 147	
Db	61	PEETVTQDCLQIADSETPTIOKGSYTFVPWLLSFKGSGALEEKENKILVKETGYFFIYG	120	
QY	148	QVLVTDKTYANGHLIQKRVHVFGEDELSTLTLFRICION-----	LESGD 190	
Db	121	QVLVTDKTYANGHLIQKRVHVFGEDELSTLTLFRICIONWPTLPNNSCYSAGIAKLESGD	180	
QY	191	ELQALAIAPRENAQIQLSDGDVTFPGALKLL	218	

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Db 181 ELQTLIPRENAQISLDGVTFFGALKLL 208
RESULT 2
Q81Z15 PRELIMINARY; PRT; 174 AA.
AC Q81Z15;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE B-lymphocyte stimulator (Fragment).
GN TNFSF13B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY129227; AAN08423.1; -.
FT NON_TER
SQ SEQUENCE 174 AA; 19479 MW; 1AEBD4F2862EB3E0 CRC64;
Query Match 60.7%; Score 677; DB 4; Length 174;
Best Local Similarity 79.8%; Pred. No. 1.7e-61;
Matches 138; Conservative 0; Mismatches 1; Indels 34; Gaps 2;
Qy 80 KIFEPAPGEGNSSNSNRKRAVQPEETVTDCLQLIADSETPTIQKSYTFVPWLLSF 139
Db 2 KIFEPAPGEGNSSNSNRKRAVQPEETVTDCLQLIADSETPTIQKSYTFVPWLLSF 61
Qy 140 KRGSL-----YGVLYTDKTYAMGHLIQRKKVHVFGEDELSTVTLPRC 182
Db 62 KRGSALEEKENKILVKGTYFYGVLYTDKTYAMGHLIQRKKVHVFGEDELSTVTLPRC 121
Qy 183 IQN-----LEEGDELOLAIPRENAQISLDGVTFFGALKLL 218
Db 122 IQNMPETLPNNSCYSAGIAKLEEGDELQITIPRENAQISLDGVTFFGALKLL 174
RESULT 3
Q8BZM8 PRELIMINARY; PRT; 258 AA.
AC Q8BZM8;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE Tumor necrosis factor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RL STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=22354683; PubMed=12468851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002).
DR EMBL; AK034121; BAC28593.1; -.
FT NON_TER
SQ SEQUENCE 258 AA; 28604 MW; E6431FE93E782810 CRC64;
Query Match 54.7%; Score 610; DB 11; Length 258;
Best Local Similarity 53.0%; Pred. No. 2.3e-54;
Matches 134; Conservative 17; Mismatches 28; Indels 74; Gaps 4;
Qy 40 LLSCCLTVVSYQVAALQGLDASLRAELQGH-----AEKLPAGAKIFEPPAPGEG 90
Db 6 LLSSSFTAMSLYQLAALQADLMNLRLWELQSYRGSAATPAAGAPELTAGVKLLTTPAAPRPH 65
Qy 91 NSSQNSNRKRAVQPEET-----VTQDCLQLIAD 119
Db 66 NSSRGRNRRAFAVQPEETQDVLSAPPAPCLPCRHSQDDHGMNLRNIIQDCLQLIAD 125
Qy 120 SETPTIQKSYTFVPWLLSFKRGSL-----YGVLYTDKTYAMGHLI 162
Db 126 SDFTIRKGYTFVPWLLSFKRGNALEKENKIVVQTGYFFIYSQVLYTDPIFAMGHVI 185
Qy 163 QRKKVHVFGEDELSTVTLPRCQN-----LEEGDELOLAIPRENAQISL 205
Db 186 QRKKVHVFGEDELSTVTLPRCQNPKTLNNSCYSAGIARLEEGDEIQLAIPRENAQISR 245
Qy 206 DGDVTFFGALKLL 218
Db 246 NGDDTFFGALKLL 258
RESULT 4
Q81Z14 PRELIMINARY; PRT; 158 AA.
AC Q81Z14;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE B-lymphocyte stimulator (Fragment).
GN TNFSF13B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RL He F., Gao H., Li R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY129228; AAN08424.1; -.
FT NON_TER
SQ SEQUENCE 158 AA; 17826 MW; 8346BCC0D333DCAB CRC64;
Query Match 53.4%; Score 596; DB 4; Length 158;
Best Local Similarity 77.8%; Pred. No. 3.2e-53;
Matches 123; Conservative 0; Mismatches 1; Indels 34; Gaps 2;
Qy 95 NSNRKRAVQPEETVTDCLQLIADSETPTIQKSYTFVPWLLSFKRGSL----- 145
Db 1 NSNRKRAVQPEETVTDCLQLIADSETPTIQKSYTFVPWLLSFKRGSALEEKENKILV 60
Qy 146 -----YGVLYTDKTYAMGHLIQRKKVHVFGEDELSTVTLPRCQN----- 185
Db 61 KETGYFYGVLYTDKTYAMGHLIQRKKVHVFGEDELSTVTLPRCQNMPETLPNNSCYS 120
Qy 186 -----LEEGDELOLAIPRENAQISLDGVTFFGALKLL 218
Db 121 AGIAKLEEGDELQITIPRENAQISLDGVTFFGALKLL 158
RESULT 5
Q8JHJ4 PRELIMINARY; PRT; 288 AA.
AC Q8JHJ4;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE TNF family B cell activation factor.
GN BAFF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Schneider K., Koltow S., Schneider P., Goebel T., Kaspers B.,
```

RA Staeheli P.;
RT "A chicken homolog of the B cell activating factor of the TNF family
(BAPF).";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF505010; AAM90951.2; -- 8E2F291D2495BB79 CRC64;
SQ SEQUENCE 288 AA; 31629 MW; 8E2F291D2495BB79 CRC64;

Query/Match 44.6%; Score 497.5; DB 13; Length 288;
Best Local Similarity 41.7%; Pred. No. 9.8e-43;
Matches 120; Conservative 28; Mismatches 49; Indels 91; Gaps 7;

QY 22 MKLKECVSLPRKE---SPS-----VLLSCCLTVSVFYVAALQ 57
DB 1 MKSVCVHVIOQKDTASSPSPPGAAGTGTGLFVTFLLWMLLSSCLAASVLYHATLK 60
QY 58 GLASLRAELQGHAEKLP-----AGAKI-----FEPPAPGE 89
DB 61 TELEALRSELIYVRVARSLEQPPVSPGDKKAGASVSSFLQVSAAGROENLPGSPAE 120
QY 90 GNSSQ-----NSRNRKAVQGPETVTQDCLQIADSETPTIQGSYTFVFWLLSFKRGA 144
DB 121 SFQTEIWDNRNRGRSIVNAETVLQACLIADSKSDIQKDDSSIVFWLLSFKRGA 180
QY 145 L-----YGVLYYDXTVAMGHLIQRKVKHVFGBELSLVTLFRQION-- 185
DB 181 LEEQGNKIVIKETGYFFIYGVLYTDTTFAMGHLIQRKKAHVFGDDLSLVTLFRQIONMP 240
QY 186 -----LEEDELQALIPRENAOISLDGVTFFGALKLL 218
DB 241 QSPYNNSCYTAGIALEGEDELQLTIPRRRAKISLDGDTFFGAVRLL 288

RESULT 6
Q8BWP2 ID Q8BWP2 PRELIMINARY; PRT; 199 AA.
AC Q8BWP2;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Tumor necrosis factor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK050384; BAC34225.1; --
SQ SEQUENCE 199 AA; 21654 MW; 39392021D4EFD320 CRC64;

Query/Match 22.6%; Score 252.5; DB 11; Length 199;
Best Local Similarity 36.9%; Pred. No. 9.4e-18;
Matches 69; Conservative 18; Mismatches 41; Indels 59; Gaps 5;

QY 1 MDDSTER-EQSRLTSLCKREEMKKECVSILPRKESPS-----VLLS 42
DB 1 MDESATLPPCLCFCESEKEDMKV-GYDPTIPQKEGAWFGICRDGRLLAATLLALLS 59
QY 43 CCLTVSVFYVAALQGDLSLRAELQGH-----AEKLPAGAKIFEPPAPGEGNSS 93
DB 60 SSFTAMSLYQLAALQADLMNLRLMELQSVRGSAAPAGAPELTAGVKLLTPAAPRPHNSS 119
QY 94 QNSRNRKAVQGPET-----VTQDCLQIADSET 122
DB 120 RGRNRRAFGPPEETEQQVDLSAPPAPCLPGCRHSQHDNDGNNLRNIITQDCLQIADSDT 179
QY 123 PTIOKGS 129
DB 180 PTIRKGN 186

RESULT 8
Q8NFH7 ID Q8NFH7 PRELIMINARY; PRT; 250 AA.
AC Q8NFH7;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Proliferation-inducing ligand APRIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyama T., Tsukamoto H., Masumoto K., Himeji D., Hayaishi K.,
RA Harada M., Horiuchi T.;
RT "Genomic structure of APRIL, a proliferation-inducing ligand.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF513501; AAM47279.1; --
DR InterPro; IPR006052; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.

```
SQ SEQUENCE 250 AA; 27453 MW; AE1E4FDEFD578898 CRC64;
Query Match 13.6%; Score 152; DB 4; Length 250;
Best Local Similarity 24.9%; Pred. No. 2.8e-07;
Matches 58; Conservative 31; Mismatches 64; Indels 80; Gaps 9;

QY 41 LSCCLTVVSFYQVAALQGDLSLRAE---LQGHAEKLPAGAKIPEPPAPGEG----- 90
DB 42 VACAWALIT-----QTELOSRLREVSRLQ-----TGG-----PSQNGEGYPWQSLP 84
QY 91 -----NSSQNSRNKRAVQGPETVTQDCLQLIADSETPTTQKGSYTFVPWLLSFK 140
DB 85 EQSSDALEAWENGERSRKRRAVLTKQKKQHSVLHVPINAT-SKDDSDVTEVMQPALR 143
QY 141 RGSAA-----LYGOVLYTDKTYANGHLIQRKKVHVGDELSLTLFRCI 183
DB 144 RGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSRE-----GQGRQETLFRCI 197
QY 184 Q-----NLEEGDELQALIPRENAQISLDGDVTFFGALKL 217
DB 198 RSMSPHPDRAYNCSYAGVFLHQDILSVIIPRARKNLSPHGTFLGFVKL 250

RESULT 9
QBX82
ID Q8BX82 PRELIMINARY; PRT; 410 AA.
AC Q8BX82;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Tumor necrosis factor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK044387; BAC31897.1; --
SQ SEQUENCE 410 AA; 45881 MW; 590A4B74C33FB8D4 CRC64;

Query Match 13.1%; Score 146; DB 11; Length 410;
Best Local Similarity 26.1%; Pred. No. 2.3e-06;
Matches 57; Conservative 24; Mismatches 71; Indels 66; Gaps 7;

QY 52 QVAALQGDLSLRAE---LQGHAEKLPAGAKIFE-----PPAPGEGNSQNSRNKRAV 102
DB 207 QLRLCQTELOSRLREVSRLQSGSPQKQGERPQWQSLMEQSDVLEAKWDGAKSRRRRAV 266
QY 103 QGPETVTQDCLQLI-----ADSETPTTQKGSYTFVPWLLSFKRGS----- 144
DB 267 LTQHKHKKHSVLHVPVNTSKADSDV-----TEVMQVLRGRGLEAQGDIVRW 318
QY 145 -----LYGOVLYTDKTYANGHLIQRKKVHVGDELSLTLFRCIQ----- 184
DB 319 DTGIVYLLYSQVLFHDVTFTMGQVVSRE-----GQGRQETLFRCI RSMSPHPDRAYNSCY 372
QY 185 -----NLEEGDELQALIPRENAQISLDGDVTFFGALKL 217
DB 373 SAGVFLHQGDIIITVKIPRANKLSLSPHGTFLGFVKL 410

RESULT 10
Q81ZK7
ID Q81ZK7 PRELIMINARY; PRT; 330 AA.
AC Q81ZK7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
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DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE TWE-PRIL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=22299924; PubMed=12411489;
RA Pradet-Balade B.; Medema J.P.; Lopez-Fraga M.; Lozano J.C.;
RA Kolfschoten G.M.; Picard A.; Martinez-A C.; Garcia-Sanz J.A.;
RA Hahne M.;
RT "An endogenous hybrid mRNA encodes TWE-PRIL, a functional cell surface
RT TWEAK-APRIL fusion protein."
RL EMBL J. 21:5711-5720 (2002).
DR EMBL; AY081051; AAL90443.1; --
SQ SEQUENCE 330 AA; 36588 MW; FC6F3BCA29C029AE CRC64;

Query Match 12.6%; Score 140.5; DB 4; Length 330;
Best Local Similarity 26.5%; Pred. No. 6.3e-06;
Matches 43; Conservative 24; Mismatches 52; Indels 43; Gaps 4;

QY 92 SSQNSRNKRAVQGPETVTQDCLQLIADSETPTTQKGSYTFVPWLLSFKRGS----- 144
DB 176 NGRSRKRRAVLTKQKKQHSVLHVPINAT-SKDDSDVTEVMQPALRRGRGLQAQGYG 234
QY 145 -----LYGOVLYTDKTYANGHLIQRKKVHVGDELSLTLFRCIQ----- 184
DB 235 VRIQDAGVYLLYSQVLFQDVTFTMGQVVSRE-----GQGRQETLFRCI RSMSPHPDRAY 288
QY 185 -----NLEEGDELQALIPRENAQISLDGDVTFFGALKL 217
DB 289 NSCVSAGVFLHQDILSVIIPRARKNLSPHGTFLGFVKL 330

RESULT 11
Q98B67
ID Q98B67 PRELIMINARY; PRT; 267 AA.
AC Q98B67;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Transcriptional regulator.
CN MLL5707.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T.; Nakamura Y.; Sato S.; Asamizu E.; Kato T.; Sasamoto S.;
RA Watanabe A.; Idesawa K.; Ishikawa A.; Kawashima K.; Kimura T.;
RA Kishida Y.; Kiyokawa C.; Kohara M.; Matsumoto M.; Mateuno A.;
RA Mochizuki Y.; Nakayama S.; Nakazaki N.; Shimpō S.; Sugimoto M.;
RA Takeuchi C.; Yamada M.; Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338 (2000).
DR EMBL; AP003007; BAB52105.1; --
DR InterPro; IPR001034; HTH_Deor.
DR Pfam; PF00455; deor; 1.
DR PRINTS; PR00037; HTHLACR.
DR SMART; SMO0420; HTH_DEOR; 1.
DR PROSITE; PS00894; HTH_DEOR_FAMILY; 1.
KW Complete proteome.
SQ SEQUENCE 267 AA; 29577 MW; 03E99717CA35F544 CRC64;

Query Match 8.2%; Score 91.5; DB 16; Length 267;
Best Local Similarity 21.2%; Pred. No. 0.51;
Matches 48; Conservative 39; Mismatches 70; Indels 69; Gaps 11;
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```
QY 6 EREQSR-LTSCLKREEMKKECVSLPKESPSVLLSCCLTVWSFYQVAALQGLASLR 64
Db 3 EKERHRIILSAVQEPVTVQEWDLTSESSE-----ATIRRDIAALH 44
QY 65 AELQGHAEKLPAGAKIFEP-----APGSGNSSQNRKRAVQGPETVTDCLQI 117
Db 45 VQ---KRLRVRGGAIAISPPFIGLAGRPFSVNETINASQKRA-----IAREAVELC 94
QY 118 ADSEPTTQKGSYTFVPMLLSKFGSALYGVLYTDKTYAMGHLLIQRKXVHVFGDELSIV 177
Db 95 GGEPIIINGGTTT---QVHFLTGRM---PFTNSPFIAPHLKHSKNTVM---LSGG 146
QY 178 TLFRCTQNLQEGDELQALPENAQIS-ILDGVDV-----FFGA 214
Db 147 TIYR-----EQNIILSPDNDVTRNFYARRFMGA 176

RESULT 12
QW2R3
ID Q8W2R3 PRELIMINARY; PRT; 695 AA.
AC Q8W2R3;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Putative wall-associated protein kinase.
GN OSJNBA0028C16.9
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Wing R.A.; Yu Y.; Soderlund C.; Chen M.; Kim H.-R.; Rambo T.;
RA Sasaki C.; Henry D.; Oates R.; Simmons J.;
RT "Rice Genomic Sequence";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC098565; AAL69427.1;
DR Gramene; Q8W2R3;
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS00010; ASX HYDROXYL; 1.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; EGF-like domain; Kinase; Transferase.
SQ SEQUENCE 695 AA; 77048 MW; D9DFE3A74A655A5 CRC64;

Query Match 8.2%; Score 91.5; DB 10; Length 695;
Best Local Similarity 27.4%; Pred. No. 1.9;
Matches 46; Conservative 26; Mismatches 77; Indels 19; Gaps 9;

QY 40 LLSCCLTV---VSFYQVAALQGLASLRAELQGHAEKLPAGAKIFEPAPGEGNSSQNS 96
Db 479 LLGCCLVDVPMVLYEFA-KGNLQDI---LHGDNAPLPGLRLNIAESAEGLRYMHS 534
QY 97 RNKRAVQGPETVTDCLQIADSETPTQKGSYTFVPMLLSKFGSALY---GVLYTDK 154
Db 535 STSRTIRHGD---VKPANILLTDKTIPIK---SYFGTSKLLTVDKDFTFVVGSMGYIDP 588
QY 155 TY-AMGHLLIQRKXVHVFGDELSIVTLFRCTQNLQEGDELQALPENA 201
Db 589 VPHKTHLTKQSDVSFG---VWLELI-CRKPTIYGENCSLIIEFQNA 633

RESULT 13
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Q9AXN0
ID Q9AXN0 PRELIMINARY; PRT; 1746 AA.
AC Q9AXN0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE DNA-dependent RNA polymerase II largest subunit RPB1.
GN RPB1.
OS Glaucosphaera vacuolata.
OC Eukaryota; Glaucocystophyceae; Gloeochaetales; Glaucosphaeraeae;
OC Glaucosphaera.
OX NCBI_TaxID=38265;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21336853; PubMed=11443356;
RA Stiller J.W.; Riley J.; Hall B.D.;
RT "Are red algae plants? A critical evaluation of three key molecular
RT data sets.";
RL J. Mol. Evol. 52:527-539 (2001).
DR EMBL; AF315820; AAK00310.1;
DR InterPro; IPR002965; P rich extensin.
DR InterPro; IPR006592; RNA_pol_A_N.
DR InterPro; IPR000684; RNA_polII_repeat.
DR InterPro; IPR000722; RNA_pol_A.
DR InterPro; IPR007080; RNA_pol_Rpb1_1.
DR InterPro; IPR007066; RNA_pol_Rpb1_3.
DR InterPro; IPR007083; RNA_pol_Rpb1_4.
DR InterPro; IPR007081; RNA_pol_Rpb1_5.
DR InterPro; IPR007075; RNA_pol_Rpb1_6.
DR InterPro; IPR007073; RNA_pol_Rpb1_7.
DR Pfam; PF04967; RNA_pol_Rpb1_1; 1.
DR Pfam; PF00623; RNA_pol_Rpb1_2; 1.
DR Pfam; PF04983; RNA_pol_Rpb1_3; 1.
DR Pfam; PF05000; RNA_pol_Rpb1_4; 1.
DR Pfam; PF04998; RNA_pol_Rpb1_5; 1.
DR Pfam; PF04992; RNA_pol_Rpb1_6; 1.
DR Pfam; PF04990; RNA_pol_Rpb1_7; 1.
DR PRINTS; PR01217; PRICHEXTENSIN.
DR SMART; SM00663; RPOLA_N; 1.
DR PROSITE; PS00115; RNA_POL_II_REPEAT; 12.
DR PROSITE; PS00115; RNA_POL_II_REPEAT; 12.
SQ SEQUENCE 1746 AA; 193767 MW; C0769A3392D6746D CRC64;

Query Match 7.9%; Score 88; DB 10; Length 1746;
Best Local Similarity 21.8%; Pred. No. 15;
Matches 42; Conservative 32; Mismatches 57; Indels 62; Gaps 10;

QY 23 KLCVCVSLPKESPSVLLSCCLTVWSFYQVAALQGLA-----SURAELOGHAEK 75
Db 1118 RLKEIINVAKCKTPS-----LTVY-----LRGEAARDAERAKQVQAELOHTLNV 1164
QY 76 PAGAKIPEPPAPGEGNSSQNSRKRKRAVQGPETVTDCLQIAD-SETPTQKGSYTFV 134
Db 1165 TQSTEIYDPP-----NPQDTVIEADQELVRSYVELPDDENSSANLSP 1206
QY 135 WLLSPKFGSALYGVLYTDKTYAMGHLLIQRKXVH---VFGD-----ELSLVTLFR 183
Db 1207 WLLRLN-----LSKEMTDRKLSMNHV---KNKIHDLGDDVNVWASENDANLVR 1259
QY 184 -----QNLREGDE 191
Db 1260 AQKEPEKMAEGEE 1272

RESULT 14
Q55896
ID Q55896 PRELIMINARY; PRT; 240 AA.
AC Q55896;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical protein slr0120.
GN SLR0120.
OS Synechocystis sp. (strain PCC 6803).
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:43:37 ; Search time 36.3333 Seconds
(without alignments)
952.359 Million cell updates/sec

Title: US-09-911-777-1
Perfect score: 1116
Sequence: 1 MDDSTERQSLTSLCKRE.....ENAIQLSDGVDVFFGALKLL 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1042.5	93.4	285	19 AAW73043	Tumour necrosis factor
2	1042.5	93.4	285	19 AAW62461	Human T cell surfa
3	1042.5	93.4	285	19 AAW58391	Homo sapiens neutr
4	1042.5	93.4	285	20 AAY22221	Human TNF11 protei
5	1042.5	93.4	285	20 AAY04392	Human Kay-ligand.
6	1042.5	93.4	285	20 AAW93586	Human TNF11-alpha
7	1042.5	93.4	285	21 AAB28553	Human TNF11. Homo
8	1042.5	93.4	285	21 AAB08659	Amino acid sequenc
9	1042.5	93.4	285	21 AAB08191	Amino acid sequenc

10	1042.5	93.4	285	21 AAB08261	Amino acid sequenc
11	1042.5	93.4	285	22 AAE09242	Human TALL-1 prote
12	1042.5	93.4	285	22 AAE07156	Human tumour necro
13	1042.5	93.4	285	22 AAE07879	Human BAPF protein
14	1042.5	93.4	285	22 AAU12183	Human PRO738 polyp
15	1042.5	93.4	285	22 AAY71915	Human TAC1-ligand
16	1042.5	93.4	285	22 AAY71978	Human TNF and Apol
17	1042.5	93.4	285	23 AAE28963	Human ZTN4 protein
18	1042.5	93.4	285	23 ABG96458	Human Neutrokine-a
19	1042.5	93.4	285	23 AAE26214	Human neutrokine-a
20	1042.5	93.4	285	23 AAE24636	Human tumour necro
21	1042.5	93.4	285	23 ABB81485	Human ZTNF4 amino
22	1042.5	93.4	285	23 ABJ00715	Human B lymphocyte
23	1042.5	93.4	285	23 ABP47217	Human Blys binding
24	1042.5	93.4	285	23 ABB95471	Human angiogenesis
25	1042.5	93.4	285	23 ABG33576	Human B lymphocyte
26	1042.5	93.4	285	23 AAU79140	Human Neutrokine-a
27	1042.5	93.4	285	23 ABB90325	Human polypeptide
28	1042.5	93.4	285	23 ABB84865	Human PRO738 prote
29	1042.5	93.4	285	23 AAU75409	Neutrokine-alpha (
30	1042.5	93.4	285	23 AAU10942	Human AGP-3. Homo
31	1042.5	93.4	285	24 ABU66581	Human PRO polypept
32	1042.5	93.4	285	24 ABU66857	Human secreted/tra
33	1042.5	93.4	285	24 AAE35212	Human tumour necro
34	1042.5	93.4	285	24 ABP97718	Amino acid sequenc
35	1042.5	93.4	285	24 ABUS9662	Novel secreted and
36	1042.5	93.4	285	24 ABP57103	Membrane bound Bly
37	1042.5	93.4	285	24 ABP60543	Human tumour necro
38	1035.5	92.8	285	21 AAY97037	Membrane bound hum
39	936.5	83.9	264	20 AAW82268	Human NTN-2 protei
40	936.5	83.9	264	20 AAW82270	Human NTN-2 DNA se
41	936.5	83.9	264	21 AAY94005	A human tnfr4, a t
42	927	83.1	266	19 AAW62462	Human T cell surfa
43	927	83.1	266	21 AAB08660	A human neutrokine
44	927	83.1	266	23 ABG96463	Human Neutrokine-a
45	927	83.1	266	23 AAE26215	Human neutrokine-a

ALIGNMENTS

RESULT 1
AAW73043
ID AAW73043 standard; Protein; 285 AA.
XX
AC AAW73043;
XX
DT 07-JAN-1999 (first entry)
XX
DE Tumour necrosis factor homologue TL5 protein.
XX
KW Tumour necrosis factor homologue TL5; vaccine; chronic;
KW acute inflammation; arthritis; septicemia; autoimmune disease;
KW inflammatory bowel disease; psoriasis; transplant rejection;
KW graft vs. host disease; infection; stroke; ischaemia;
KW acute respirator disease syndrome; testonosis; brain injury; AIDS;
KW bone disease; cancer; lymphoproliferative disorder; atherosclerosis;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN EP869180-A1.
XX
PD 07-OCT-1998.
XX
PF 01-APR-1998; 98EP-0302526.
XX
PR 03-DEC-1997; 97US-0984396.
XX
PR 02-APR-1997; 97US-0041797.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Hurle MR, Young PR;

XX WPI; 1998-508494/44.
 DR N-PSDB; AAV58894.
 XX
 XX New tumour necrosis factor homologue, TL5 - useful for diagnosis and
 PT treatment of Alzheimer's disease, AIDS and cancer
 XX
 XX
 PS Claim 10; Page 18; 23pp; English.
 XX
 XX The present sequence encodes a tumour necrosis factor homologue TL5
 CC polypeptide sequence. TL5 polypeptides and antibodies are useful for
 CC identifying compounds which agonise and antagonise TL5, and these can be
 CC administered for treatment to inhibit TL5 activity (antagonist) or
 CC enhance TL5 activity (agonist). Gene therapy using the expression system
 CC can also be used to enhance TL5 activity. Diseases or susceptibility to a
 CC disease can be diagnosed by determining the presence or absence of a
 CC mutation in the TL5 protein. TL5 polynucleotides are useful for locating
 CC genes associated with disease by hybridisation to chromosomes. TL5
 CC polypeptides and polynucleotides can be used, especially to raise an
 CC immune response (i.e. as vaccines) for the treatment of chronic and acute
 CC inflammation, arthritis, septicemia, autoimmune diseases (e.g.
 CC inflammatory bowel disease, psoriasis), transplant rejection,
 CC graft vs. host disease, infection, stroke, ischaemia, acute respiratory
 CC disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer
 CC (e.g. lymphoproliferative disorders), atherosclerosis, and Alzheimers
 CC disease.
 XX
 SQ Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 19; Length 285;
 Best Local Similarity 76.5%; Pred. No. 1.1e-103;
 Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
 QY 1 MDDSTERQSLTSLCKREEMKKECVSILPRKESPSV-----LLSCC 44
 DB 1 MDDSTERQSLTSLCKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
 QY 45 LTVVSFYQVAALQGLDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
 DB 61 LTVVSFYQVAALQGLDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
 QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSALE 145
 DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSALE 180
 QY 146 -----YGOVLYTDKTYAMGHLIQKRVHVFGEDELSTVTLFRCIQN----- 185
 DB 181 KENKILVKETGYFFIYQVLYTDKTYAMGHLIQKRVHVFGEDELSTVTLFRCIQNMPETL 240
 QY 186 -----LEEGDELQLAIPRENAQISLDGDTFFFGALKLL 218
 DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFFGALKLL 285

RESULT 2
 AAW62461
 ID AAW62461 standard; Protein; 285 AA.
 XX
 AC AAW62461;
 XX
 XX 05-OCT-1998 (first entry)
 DT
 XX
 XX Human T cell surface antigen 63954 protein sequence #2.
 DE
 XX Human; 63954; primate; rodent; mouse; T cell surface antigen; mammal;
 KW diagnosis; antigen-specific proliferation; cytokine production;
 KW immune response; autoimmune disorder; rheumatoid arthritis;
 KW systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis.
 XX
 OS Homo sapiens.
 XX
 PN W09827114-A2.
 XX

PD 25-JUN-1998.
 XX
 XX 16-DEC-1997; 97WO-US23321.
 XX
 XX 17-DEC-1996; 96US-0033601.
 XX
 XX (SCHE) SCHERING CORP.
 XX
 XX Gorman DM;
 XX
 XX WPI; 1998-362719/31.
 DR N-PSDB; AAV39985.
 XX
 XX New isolated polypeptide, 63954 - used to develop products for
 PT treating e.g. autoimmune disorders, inflammation, tissue rejection,
 PT cancer or degenerative conditions
 XX
 XX Claim 1; Page 60-61; 69pp; English.
 XX
 XX The present sequence is a human T cell surface antigen, designated
 CC 63954. The novel protein designated 63954 is expressed on T cells.
 CC Protein 63954 can modulate antigen-specific proliferation and cytokine
 CC production on effector cells and may potentiate immune cell expansion or
 CC apoptosis. 63954 agonists or antagonists may also act as a co-stimulatory
 CC molecule for regulation of T cell mediated cell activation, and may cause
 CC a shift of T helper cell types, e.g. between Th1 and Th2. Antagonists of
 CC 63954 can be used to modulate immune responses in abnormal situations,
 CC e.g. autoimmune disorders, including rheumatoid arthritis, systemic
 CC lupus erythematosus (SLE), Hashimoto's autoimmune thyroiditis, as well
 CC as acute and chronic inflammatory responses in which T cell activation,
 CC expansion, and/or immunological T cell memory play an important role,
 CC such as chronic inflammation or tissue rejection. The products can also
 CC be used in the treatment of conditions associated with abnormal
 CC physiology or development, including abnormal proliferation, e.g.
 CC cancerous conditions, or degenerative conditions. The products can also
 CC be used for detection, diagnosis and drug screening.
 XX
 SQ Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 19; Length 285;
 Best Local Similarity 76.5%; Pred. No. 1.1e-103;
 Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
 QY 1 MDDSTERQSLTSLCKREEMKKECVSILPRKESPSV-----LLSCC 44
 DB 1 MDDSTERQSLTSLCKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
 QY 45 LTVVSFYQVAALQGLDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
 DB 61 LTVVSFYQVAALQGLDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
 QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSALE 145
 DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSALE 180
 QY 146 -----YGOVLYTDKTYAMGHLIQKRVHVFGEDELSTVTLFRCIQN----- 185
 DB 181 KENKILVKETGYFFIYQVLYTDKTYAMGHLIQKRVHVFGEDELSTVTLFRCIQNMPETL 240
 QY 186 -----LEEGDELQLAIPRENAQISLDGDTFFFGALKLL 218
 DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFFGALKLL 285

RESULT 3
 AAW58391
 ID AAW58391 standard; Protein; 285 AA.
 XX
 AC AAW58391;
 XX
 XX 11-SEP-1998 (first entry)
 DT
 XX
 XX Homo sapiens neutrokin alpha protein.

XX neurokine alpha; cell proliferation; differentiation; migration;
 KW cytotoxicity; cell death; treatment; tumour; infection; inflammation;
 KW wound healing; immunodeficiency; autoimmune disease; graft rejection;
 KW fibrotic disorder; haematopoiesis; sepsis; shock; malaria; HIV; AIDS;
 KW acquired immune deficiency syndrome; rheumatoid arthritis; silicosis;
 XX cachexia; detection; diagnosis; drug screening.

XX Homo sapiens.

OS Key Location/Qualifiers
 FT Domain 1..46
 FT /note= "intracellular domain"
 FT 47..72
 FT /note= "transmembrane domain"
 FT 73..285
 FT /note= "extracellular domain"

XX WO9818921-A1.
 XX
 XX 07-MAY-1998.
 XX
 XX 25-OCT-1996; 96WO-US17957.
 XX
 XX 25-OCT-1996; 96WO-US17957.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ebner R, Ni J, Yu G;
 XX
 XX WPI; 1998-272216/24.
 XX N-PSDB; AAV30934.

XX New isolated human Neurokine alpha - used to develop products for
 PT diagnosis and treatment of e.g. tumours, infections,
 PT immunodeficiencies or autoimmune diseases

XX Claim 17; Fig 1; 104pp; English.

XX The sequence is that of the neurokine alpha protein.

CC Neurokine alpha (NA) polypeptides modulate cell proliferation,
 CC differentiation, migration, cytotoxicity and cell death.
 CC They can be used to treat e.g. tumour and tumour metastasis, infections
 CC by bacteria, viruses and other parasites, immunodeficiencies,
 CC inflammatory diseases, lymphadenopathy, autoimmune diseases, graft
 CC versus host disease and to stimulate peripheral tolerance, destroy some
 CC transformed cell lines, mediate cell activation and proliferation, and
 CC are functionally linked as primary mediators of immune regulation and
 CC inflammatory responses. Such activity is useful for immune enhancement
 CC or suppression, myelopoietic, stem cell mobilisation, acute and
 CC chronic inflammatory control and treatment of leukaemia. They can also
 CC be used to stimulate wound healing and to treat fibrotic disorders
 CC including liver cirrhosis, osteoarthritis and pulmonary fibrosis. They
 CC can also be used to regulate haematopoiesis, by regulating the activation
 CC and differentiation of various haematopoietic progenitor cells, e.g. to
 CC release mature leukocytes from the bone marrow following chemotherapy, NA
 CC and in stem cell mobilisation. NA may also be used to treat sepsis. NA
 CC antagonists can be used to prevent septic shock, inflammation, cerebral
 CC malaria, activation of the HIV virus, graft-host rejection, bone
 CC resorption, rheumatoid arthritis and cachexia (wasting or malnutrition).
 CC They can also be used to treat e.g. autoimmune diseases such as multiple
 CC sclerosis and insulin-dependent diabetes and inflammatory and infectious
 CC diseases such as silicosis, and sarcoidosis, idiopathic pulmonary
 CC fibrosis, idiopathic hyper-eosinophilic syndrome, endotoxic shock,
 CC atherosclerosis, histamine-mediated allergic reactions and immunological
 CC disorders including late phase allergic reactions, chronic urticaria, and
 CC atopic dermatitis by inhibiting chemokine-induced mast cell and basophil
 CC degranulation and release of histamine. Ige-mediated allergic reactions
 CC such as allergic asthma, rhinitis and eczema, inflammatory pulmonary
 CC diseases, rheumatoid arthritis, inflammation, degenerative and
 CC inflammatory arthropathies, aplastic anaemia, myelodysplastic syndrome,
 CC subepithelial basement membrane fibrosis or adult respiratory distress
 CC syndrome. The products can also be used for detection, diagnosis and

CC drug screening.
 XX
 XX Sequence 285 AA;
 Query Match 93.4%; Score 1042.5; DB 19; Length 285;
 Best Local Similarity 76.5%; Pred. No. 1.1e-103;
 Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCLEKREMKLKECVSILPRKESPSV-----LLSCL 44
 |||||
 DB 1 MDDSTEREQSLTSCLEKREMKLKECVSILPRKESPSVRSKDKGLLAALLALLSCL 60
 |||||

QY 45 LTVVSFYQVAALQGLDLSRAELQGHAEKLPAGA-----KIPEPPAP 87
 |||||
 DB 61 LTVVSFYQVAALQGLDLSRAELQGHAEKLPAGAPKAGLEBAPAVTAGIKIPEPPAP 120
 |||||

QY 88 GEGNSSQNRNKRVAQGPETVTQDCLQIADSETPTIQKSYTFVPMLLSFKRGSAL-- 145
 |||||
 DB 121 GEGNSSQNRNKRVAQGPETVTQDCLQIADSETPTIQKSYTFVPMLLSFKRGSAL-- 180
 |||||

QY 146 -----YQVLYTDKTYAMGHLIQRKQVHVFGDELSTLTPRCION----- 185
 |||||

DB 181 KENKILVKETGYFFIYQVLYTDKTYAMGHLIQRKQVHVFGDELSTLTPRCIONMPETL 240
 |||||

QY 186 -----LREGDELQAIIPRENAQISLDGDTFFFGALKLL 218
 |||||

DB 241 PNNSCYSAGIAKLEGEDELQAIIPRENAQISLDGDTFFFGALKLL 285
 |||||

RESULT 4

AAAY22221
 ID AAY22221 standard; Protein; 285 AA.

AC AAY22221;

DT 16-SBP-1999 (first entry)

DE Human TNFL1 protein sequence.

XX TNFL1; human; TNFR superfamily; tumour necrosis factor ligand; TNF;
 KW tumour necrosis factor receptor; TNFR superfamily; cell proliferation;
 KW cell differentiation; cytokine production; immunoglobulin; hyperplasia;
 KW apoptosis inducer; activated T cell; autoimmune disease; inhibitor;
 KW myasthenia gravis; insulin-dependent diabetes mellitus; endotoxic shock;
 KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
 KW tumour; proliferative disorder; neoplasia; dysplasia; immunocompetence;
 KW lymphoid organogenesis; bacterial resistance; contact hypersensitivity;
 XX delayed type sensitivity; therapy.

OS Homo sapiens.

XX WO9933980-A2.

XX 08-JUL-1999.

XX 22-DEC-1998; 98WO-US27474.

XX 16-DEC-1998; 98US-0212270.

XX 30-DEC-1997; 97US-0068959.

XX (CHIR) CHIRON CORP.

XX Kassam A, Lamson G, Pot D, Tribouley C;

XX WPI; 1999-405508/34.

XX N-PSDB; AAX84620.

XX New tumour necrosis factor ligands, useful for induction of cell
 XX death and/or proliferation of cells

XX Claim 1; Page 61; 69pp; English.

XX This sequence is the tumour necrosis factor (TNF) ligand family

protein of the invention, designated TNFL1. The TNFL proteins play regulatory roles in cell proliferation and/or differentiation, e.g. they can induce production of cytokines, immunoglobulins, etc. A variety of diseases can be treated by modulating the activity of TNFL proteins, e.g. they can induce apoptosis of activated T cells but rescue resting T cell from apoptosis. TNFL polypeptides can therefore be used to treat autoimmune diseases, such as myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus. TNFL proteins also have tumour stimulating properties, so tumours can be treated by inhibiting the expression or activity of TNFL. Other proliferative disorders, such as neoplasias, dysplasias, and hyperplasia can also be treated using TNFL inhibitors. The TNFL polypeptides and polynucleotides can also be used to enhance or decrease TNF activity, thus providing therapeutic benefits such as induction of cell death, lymphoid organogenesis, or host bacterial resistance, and inhibition of endotoxin shock, contact hypersensitivity, delayed type sensitivity or immunocompetence of a transplant recipient. Tumour necrosis factor (TNF) and its receptors play a major role in host defence and immunosurveillance. As such, there is a need to identify new members of TNFR families. This invention provides this need.

SQ Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 20; Length 285;

Best Local Similarity 76.5%; Pred. No. 1.1e-103;

Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
 DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRRSSKDGKLLAATLLALLSCC 60
 QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPAP 87
 DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
 QY 88 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSALE 145
 DB 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSALE 180
 QY 146 -----YGVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFRFCION----- 185
 DB 181 KENKILVKETGYFFIYQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFRFCIONMPETL 240
 QY 186 -----LEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 218
 DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285

RESULT 5

AAV04392

ID AAY04392 standard; Protein; 285 AA.

AC AAY04392;

DT 24-JUN-1999 (first entry)

DE Human Kay-ligand.

KW Kay-ligand; tumour necrosis factor family; TNF; immune system;
 XX cytokine; autoimmune disease; tissue graft; cancer; cell death.

OS Homo sapiens.

PN WO9112964-A2.

PD 18-MAR-1999.

PF 11-SEP-1998; 98WO-US19037.

PR 12-SEP-1997; 97US-0058786.

PA (BIOJ) BIOGEN INC.

XX

PI Tschopp J;

DR WPI; 1999-243715/20.
 DR N-PSDB; AAX33330.

XX

PT New human or murine Kay-ligands, members of the tumour necrosis
 factor family

XX

PS Claim 12; Page 32; 41pp; English.

XX

CC The present sequence represents human Kay-ligand, which is a member of
 the tumour necrosis factor (TNF) family of cytokines. Pharmaceutical
 compositions containing the Kay-ligand can be used to suppress or
 stimulate the immune system, especially to prevent or reduce the
 severity of autoimmune diseases or response to a tissue graft or to
 treat cancer. An agent capable of interfering with the Kay-ligand can be
 used to induce cell death. The Kay-ligand can also be used to identify
 its receptors.

XX

SQ Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 20; Length 285;

Best Local Similarity 76.5%; Pred. No. 1.1e-103;

Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
 DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRRSSKDGKLLAATLLALLSCC 60
 QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPAP 87
 DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
 QY 88 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSALE 145
 DB 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSALE 180
 QY 146 -----YGVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFRFCION----- 185
 DB 181 KENKILVKETGYFFIYQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFRFCIONMPETL 240
 QY 186 -----LEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 218
 DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285

RESULT 6

AAW93586

ID AAW93586 standard; Protein; 285 AA.

AC AAW93586;

DT 18-JUN-1999 (first entry)

DE Human TNRL1-alpha protein.

KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
 KW developmental abnormality; gestational abnormality; prostate cancer;
 KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
 KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
 KW apoptosis; human; TNRL1-alpha.

OS Homo sapiens.

PN WO9111791-A2.

PD 11-MAR-1999.

PF 04-SEP-1998; 98WO-US18393.

PR 05-SEP-1997; 97US-0924634.

PA (UNIW) UNIV WASHINGTON.

XX

XX Chaudhary PM;
 XX WPI; 1999-205191/17.
 DR N-PSDB; AAX23420.
 XX New Tumor Necrosis Factor family receptor polypeptides and ligands -
 PT useful for diagnosis and treatment of prostate cancer and
 PT developmental or gestational abnormalities
 XX
 XX Claim 34; Fig 11A; 156pp; English.
 XX
 XX This invention describes isolated Tumor Necrosis Factor (TNF) family
 CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
 CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
 CC their active fragments. APO4 is useful for diagnosing prostate cancer
 CC by determining levels of APO4 in an individual. Prostate cancer can also
 CC be treated using APO4 selective binding agents linked to a therapeutic
 CC moiety. APO4 polypeptides are also useful for identifying selective
 CC binding agents, useful in diagnosis/treatment of disease by binding of
 CC agents to the polypeptide/active fragment which is extracellular, or
 CC expressed on the cell surface. The binding is preferably performed in
 CC vivo. APO4 polypeptides/active fragments are also useful for screening
 CC for agonists and antagonists by binding and observing the change in APO4
 CC activity. Effective pharmacological agents useful in diagnosis or
 CC treatment of disease are also identified using APO4 polypeptides/active
 CC fragments and APO4 signal transducer molecules that specifically interact
 CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
 CC activity. The method is performed in vivo or in vitro. APO polypeptides
 CC are all useful as immunogens for preparing antibodies. APO4 is also
 CC useful for diagnosis/treatment of developmental or gestational
 CC abnormalities. APO8 was transfected to human breast carcinoma cell line
 CC MCF-7, and induced apoptosis.
 XX
 XX Sequence 285 AA;
 SQ

Query Match 93.4%; Score 1042.5; DB 20; Length 285;
 Best Local Similarity 76.5%; Pred. No. 1.1e-103;
 Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
 DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
 QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPAP 87
 DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGIKIFEPAP 120
 QY 88 GEGNSSQNSNRKRAVOGPEETVTDCLQIADSETPTIQKGYTFVPWLLSFKRGSAL-- 145
 DB 121 GEGNSSQNSNRKRAVOGPEETVTDCLQIADSETPTIQKGYTFVPWLLSFKRGSAL-- 180
 QY 146 -----YGVLYTDKTYAMGHLIQRKVVHVFGEDELSTLTLFRCIQN----- 185
 DB 181 KENKILVKETGYFFTYGVLYTDKTYAMGHLIQRKVVHVFGEDELSTLTLFRCIQNMPETL 240
 QY 186 -----LEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 218
 DB 241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285

RESULT 7
 ID AAB28553
 XX AAB28553 standard; protein; 285 AA.
 AC AAB28553;
 XX
 XX 08-FEB-2001 (first entry)
 DT
 XX Human TNFL1.
 DE
 XX Human; tumour necrosis factor like-1; TNFL1; tumour necrosis factor; TNF;
 KW immunosuppressive; antiarthritic; neuroprotective; dermatological;

KW antiinflammatory; antidiabetic; cytostatic; osteopathic; gene therapy;
 KW colon cancer; rheumatoid arthritis; septic shock; Crohn's disease;
 KW osteoporosis; autoimmune disease; myasthenia gravis;
 KW insulin-dependent diabetes mellitus.
 XX Homo sapiens.
 OS
 XX WO2000060079-A2.
 PN
 XX 12-OCT-2000.
 PD
 XX 05-APR-2000; 2000WO-US09059.
 PF
 XX 05-APR-1999; 99US-0286529.
 PR
 XX (CHIR) CHIRON CORP.
 PA
 XX Tribouley C;
 PI
 XX WPI; 2000-665004/64.
 DR
 XX N-PSDB; AAC63756.
 XX
 XX Tumor necrosis factor (TNF) and TNF receptor superfamily protein
 PT members TNF-L and TNFR-L, useful for enhancing or decreasing TNF
 PT activities such as inducing cell death and lymphoid organogenesis
 PS
 XX Claim 1; Page 65; 77pp; English.
 XX
 XX The present sequence is given in a specification relating to an isolated
 CC human protein designated tumour necrosis factor like-1 (TNFL1). It may be
 CC used to induce cell death in tumours, to induce apoptosis of activated T
 CC cells, to induce inflammation, and to rescue resting T cells from
 CC apoptosis. TNF receptors are used to regulate the function of a TNF
 CC ligand which plays a role in apoptosis, inflammation, differentiation, or
 CC proliferation. Expression of the receptors can also be useful as markers
 CC for cancer, especially for colon cancer. Diseases which can be treated
 CC using ligands and/or receptors of the TNF/TNFR superfamily include
 CC rheumatoid arthritis, cancer, septic shock, Crohn's disease and
 CC osteoporosis. The polynucleotides can be used in gene delivery vehicles,
 CC for the purpose of delivering a mRNA or oligonucleotide, full-length
 CC protein, fusion protein, polypeptide, or ribozyme, or single-chain
 CC antibody, into a cell. The newly identified receptor proteins play
 CC regulatory roles in cell proliferation and/or differentiation. The
 CC receptors can also play a role in the negative regulation of
 CC osteoclastogenesis. Soluble TNFR-like receptors can be useful in the
 CC neutralisation of TNF or TNF-like ligands. A TNF-L protein can also be
 CC used to treat autoimmune diseases (myasthenia gravis and
 CC insulin-dependent diabetes mellitus), tumours, and proliferative
 CC disorders. A TNF-L or TNFR-L subgenomic polynucleotide can also be
 CC delivered to subjects for the purpose of screening test compounds for
 CC those which are useful for enhancing transfer of TNF-L subgenomic
 CC polynucleotides to the cell or for enhancing subsequent biological
 CC effects of TNF-L or TNFR-L subgenomic polynucleotides within the cell.

Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 21; Length 285;
 Best Local Similarity 76.5%; Pred. No. 1.1e-103;
 Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
 DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
 QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPAP 87
 DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGIKIFEPAP 120
 QY 88 GEGNSSQNSNRKRAVOGPEETVTDCLQIADSETPTIQKGYTFVPWLLSFKRGSAL-- 145
 DB 121 GEGNSSQNSNRKRAVOGPEETVTDCLQIADSETPTIQKGYTFVPWLLSFKRGSAL-- 180
 QY 146 -----YGVLYTDKTYAMGHLIQRKVVHVFGEDELSTLTLFRCIQN----- 185

Db 181 KENKILVKETGYFFTYGQVLYTDKTYAMGHILQKRVHVFGEDELSTLFRFCIONMPETL 240
Qy 186 -----LEEGDELQAIIPRENAQISLDGVTFFGALKLL 218
Db 241 PNNCSYAGIAKLEEGDELQAIIPRENAQISLDGVTFFGALKLL 285

RESULT 8
AAB08659
ID AAB08659 standard; Protein; 285 AA.
AC AAB08659;
XX
DT 02-JAN-2001 (first entry)
XX
DE Amino acid sequence of a human neutrokinine-alpha polypeptide.
XX
KW Human; neutrokinine-alpha; tumor; tumor metastasis; infection;
KW immunodeficiency; inflammatory disease; lymphadenopathy; dermatitis;
KW autoimmune disease; graft versus host disease; immune regulation;
KW severe combined immunodeficiency-X-linked agammaglobulinemia;
KW kappa chain deficiency; B cell lymphoproliferative disorder; purpura;
KW Wiskott-Aldrich syndrome; systemic lupus erythematosus; myocarditis;
KW idiopathic thrombocytopenia purpura; hemolytic anemia; neuritis;
KW allergic encephalomyelitis; relapsing polychondritis; glomerulonephritis;
KW rheumatic heart disease; multiple sclerosis; uveitis; ophthalmia;
KW polyendocrinopathy; Reiter's disease; autoimmune pulmonary inflammation;
KW myeloprotection; stem cell mobilization; leukemia.

XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..46
FT /note= "intracellular domain"
FT Domain 47..72
FT /note= "transmembrane domain"
FT Domain 73..285
FT /note= "extracellular domain"
FT Modified-site 124..127
FT /note= "potential N-linked glycosylation site"
FT Modified-site 242..245
FT /note= "potential N-linked glycosylation site"
XX
PN WO200050597-A2.
PD 31-AUG-2000.
XX
PF 22-FEB-2000; 2000WO-US04336.
XX
PR 23-FEB-1999; 99US-0255794.
PR 02-MAR-1999; 99US-0123388.
PR 12-MAR-1999; 99US-0124097.
PR 26-MAR-1999; 99US-0126599.
PR 02-APR-1999; 99US-0127598.
PR 16-APR-1999; 99US-0130412.
PR 23-APR-1999; 99US-0130696.
PR 27-APR-1999; 99US-0131278.
PR 29-APR-1999; 99US-0131673.
PR 28-MAY-1999; 99US-0136784.
PR 06-JUL-1999; 99US-0142659.
PR 27-JUL-1999; 99US-0145824.
PR 24-NOV-1999; 99US-0167239.
PR 03-DEC-1999; 99US-0168624.
PR 16-DEC-1999; 99US-0171108.
PR 23-DEC-1999; 99US-0171626.
PR 14-JAN-2000; 2000US-0176015.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ni J, Ebner R, Yu G;
XX
DR WPI; 2000-572093/53.

DR N-ESDB; AAA64427.
XX Novel cytokine neutrokinine-alpha, its splicing variant, neutrokinine-alpha
XX SV polypeptides useful for treating tumor, tumor metastasis, microbial
PT infections, immunodeficiency, inflammatory diseases, lymphadenopathy
PT
PS Claim 18; Fig 1A-B; 414pp; English.
XX
XX The present sequence represents a human neutrokinine-alpha polypeptide.
CC Neutrokinine-alpha polypeptides are used to treat, prevent, prognosis and
CC diagnose tumor and tumor metastasis, infections by bacteria, viruses
CC and other parasites, immunodeficiencies, inflammatory diseases,
CC lymphadenopathy, autoimmune diseases, graft versus host disease, to
CC mediate immune regulation and inflammatory responses. Diseases which
CC may be treated include severe combined immunodeficiency (SCID)-X-linked
CC agammaglobulinemia, kappa chain deficiency, B cell lymphoproliferative
CC disorder (BLPD), Wiskott-Aldrich syndrome, systemic lupus erythematosus,
CC idiopathic thrombocytopenia purpura, hemolytic anemia, dermatitis,
CC allergic encephalomyelitis, myocarditis, relapsing polychondritis,
CC rheumatic heart disease, glomerulonephritis, multiple sclerosis,
CC Neuritis, Uveitis Ophthalmia, Polyendocrinopathies, Purpura
CC (e.g. Henoch-Schoenlein purpura), Reiter's Disease, and Autoimmune
CC Pulmonary Inflammation. Neutrokinine-alpha is useful for immune
CC enhancement or suppression, myeloprotection, stem cell mobilization,
XX acute and chronic inflammatory control and treatment of leukemia.
SQ Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 21; Length 285;
Best Local Similarity 76.5%; Pred. No. 1.1e-103;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
Qy 1 MDDSTEREQSLTSCLEKREMKLKECVSILPRKESPSV-----LISCC 44
Db 1 MDDSTEREQSLTSCLEKREMKLKECVSILPRKESPSVSSKDKGLAATLLALUSCC 60
Qy 45 LTVVSFYQVAALQDGLASLRAELQGHAEKLPAGA-----KIFEPAP 87
Db 61 LTVVSFYQVAALQDGLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
Qy 88 GEGNSSQNSNRKRAVQGPETVTQDCLQIADSTPTIQKSYTFVPWLLSFKGSAL-- 145
Db 121 GEGNSSQNSNRKRAVQGPETVTQDCLQIADSTPTIQKSYTFVPWLLSFKGSAL 180
Qy 146 -----YGOVLYTDKTYAMGHILQKRVHVFGEDELSTLFRFCION----- 185
Db 181 KENKILVKETGYFFTYGQVLYTDKTYAMGHILQKRVHVFGEDELSTLFRFCIONMPETL 240
Qy 186 -----LEEGDELQAIIPRENAQISLDGVTFFGALKLL 218
Db 241 PNNCSYAGIAKLEEGDELQAIIPRENAQISLDGVTFFGALKLL 285

RESULT 9
AAB08191
ID AAB08191 standard; Protein; 285 AA.
XX
AC AAB08191;
XX
DT 04-DEC-2000 (first entry)
XX
DE Amino acid sequence of human cytokine designated THANK.
XX
KW Human; cytokine; THANK; tumour necrosis factor homologue; apoptosis;
KW nuclear factor-KB; c-jun N-terminal kinase; shock; acute phase response;
KW viral infection; radiation susceptibility; atherosclerosis; cancer;
KW acute inflammatory condition; arthritis; allergy;
KW graft versus host reaction; tumour cell.

XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH

FT Domain 1..46
FT /note= "intracellular domain"
FT Domain 47..77
FT /note= "transmembrane domain"
FT Domain 78..111
FT /note= "extracellular domain"
FT Domain 112..285
FT /note= "extracellular domain"
XX WO200045836-A1.
XX
XX
XX 10-AUG-2000.
XX
XX 02-FEB-2000; 2000WO-US02751.
XX
XX 02-FEB-1999; 99US-0118531.
XX
XX (RERE-) RES DEV FOUND.
XX
XX Aggarwal BB;
XX
XX WPI; 2000-514890/46.
XX
XX
XX Inhibiting the activation of nuclear factor-kB in cells for treating
PT pathological conditions comprises treating cells with a tumour necrosis
PT factor homolog inhibitor
XX
XX
XX Example 1; Fig 1; 45pp; English.
XX
XX The present sequence represents a human cytokine, designated THANK.
CC THANK is a tumour necrosis factor (TNF) homologue that activates
CC apoptosis, nuclear factor-kB, and c-Jun N-terminal kinase. Inhibitors of
CC the THANK polypeptide are used to inhibit the activation of nuclear
CC factor-kB in cells. The method is used to inhibit the activation of
CC nuclear factor-kB in cells, treat pathological conditions such as toxic
CC and septic shock, acute phase response, viral infection, radiation
CC susceptibility, atherosclerosis, cancer, acute inflammatory conditions,
CC arthritis, allergy, and graft versus host reaction, and inhibit growth
CC of tumour cells such as myeloid cells, colon cancer cells, prostate
CC cancer cells, cervical carcinoma cells, chronic myeloid leukemic cells
CC and acute myeloid leukemic cells.
XX
XX Sequence 285 AA;
SQ
Query Match 93.4%; Score 1042.5; DB 21; Length 285;
Best Local Similarity 76.5%; Pred. No. 1.1e-103;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDKGLAATLLALLSCC 60
QY 45 LTVVSFYQVAALQGLDLSLRAELQGHAEKLPAGA-----KIFEPAP 87
DB 61 LTVVSFYQVAALQGLDLSLRAELQGHAEKLPAGAPAGKAGLEAPAVTAGLKIFEPAP 120
QY 88 GEGNSQNSRNRKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSFKRGSAL-- 145
DB 121 GEGNSQNSRNRKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSFKRGSAL 180
QY 146 -----YGVLYTDKTYAMGHLIQRKKVHVFQDELSTLFRQION----- 185
DB 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLIQRKKVHVFQDELSTLFRQIONMPTL 240
QY 186 -----LESGDELOLAI PRENAQISLDGDVTFPGALKLL 218
DB 241 PNNCSYAGIAKLESGDELOLAI PRENAQISLDGDVTFPGALKLL 285
RESULT 10
AAB08261
ID AAB08261 standard; Protein; 285 AA.
XX

AC AAB08261;
XX
XX 04-DEC-2000 (first entry)
XX
XX Amino acid sequence of a human AGP-3 polypeptide.
XX
XX AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
KW type II transmembrane protein; B cell stimulatory factor;
KW inflammatory disorder; immune disorder; rheumatoid arthritis;
KW lupus and graft versus host disease.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Domain 1..46
FT /note= "intracellular domain"
FT Region 42..72
FT /note= "transmembrane region"
FT Domain 73..285
FT /note= "extracellular domain"
XX
XX WO200047740-A2.
XX
XX 17-AUG-2000.
XX
XX 11-FEB-2000; 2000WO-US03653.
XX
XX 12-FEB-1999; 99US-0119906.
XX 18-NOV-1999; 99US-0166271.
XX (AMGE-) AMGEN INC.
XX Boyle WJ, Hsu H;
XX WPI; 2000-558217/51.
XX N-PSDB; AAA63941.
XX Novel polypeptides comprising tumour necrosis factor ligand family
PT proteins, useful for treating inflammatory and immune disorders, e.g.
PT rheumatoid arthritis
XX
XX Claim 4; Fig 1; 71pp; English.
XX
XX The present sequence represents a human AGP-3 polypeptide. AGP-3 is a
CC tumour necrosis factor (TNF) ligand family member. AGP-3 is a type II
CC transmembrane protein, and is a potent B cell stimulatory factor.
CC Expression of AGP-3 correlates to increases in the number of B cells
CC and immunoglobulins produced. AGP-3 proteins, antibodies, and nucleic
CC acids may be used to treat inflammatory and immune disorders,
CC e.g. rheumatoid arthritis, Crohn's disease, lupus and graft versus
CC host disease. The nucleic acids may be used to regulate the expression
CC of an AGP-3 related protein. The AGP-3 proteins, antibodies and nucleic
CC acids are also useful for the detection of AGP-3 agonists, antagonists
CC and characterizing interactions with AGP-3 related proteins.
CC note: this sequence is not specifically claimed. It is only mentioned
CC in the claims, in that a polypeptide that does not comprise the present
CC sequence is claimed.
XX
XX Sequence 285 AA;
SQ
Query Match 93.4%; Score 1042.5; DB 21; Length 285;
Best Local Similarity 76.5%; Pred. No. 1.1e-103;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDKGLAATLLALLSCC 60
QY 45 LTVVSFYQVAALQGLDLSLRAELQGHAEKLPAGA-----KIFEPAP 87
DB 61 LTVVSFYQVAALQGLDLSLRAELQGHAEKLPAGAPAGKAGLEAPAVTAGLKIFEPAP 120
QY 88 GEGNSQNSRNRKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSFKRGSAL-- 145

```

Db 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPPWLLSFKRGSALEE 180
Qy 146 -----YGVLYTDTKYANGHLIQRKKVHVFDELSLVTLPFCION----- 185
Db 181 KENKILVKETGYFFIYGVLYTDTKYANGHLIQRKKVHVFDELSLVTLPFCIONMPETL 240
Qy 186 -----LEEGDELQLAIPRENAQISLDGDVTFFGALKLL 218
Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285

RESULT 11
AAE09242
ID AAE09242 standard; Protein; 285 AA.
AC AAE09242;
XX
DT 19-NOV-2001 (first entry)
DE Human TALL-1 protein.
DE KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW psoriasis.
KW
OS Homo sapiens.
XX
PN WO200160397-A1.
XX
PD 23-AUG-2001.
XX
PF 28-NOV-2000; 2000WO-US32378.
XX
PR 16-FEB-2000; 2000US-0182938.
PR 22-AUG-2000; 2000US-0226986.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
PI Yan W;
XX
DR WPI; 2001-541628/60.
DR N-PSDB; AAD15903.
XX
PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity, for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists -
XX
PS Claim 2; Fig 3; 160pp; English.
XX
CC The invention relates to methods of using one or more agonists or
CC antagonists to modulate the activity of the members of TNF (tumour
CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
CC e.g. TACI or BCMA. The method is useful for treating pathological
CC conditions or diseases associated with increased TALL-1 and APRIL
CC expression or activity. TALL-1 and APRIL antagonists are used to
CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
CC They are useful for treating a mammal suffering from cancer such
CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
CC psoriasis and lupus erythematosus. The present sequence is human
CC TALL-1 protein.
XX
SQ Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 22; Length 285;
Best Local Similarity 76.5%; Pred. No. 1.1e-103;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

Qy 1 MDDSTEREQSLTSCLEKREEMKLEKCVSLPRKESPSVRSSKDGKLLAATLLALLUSCC 44

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Db 1 MDDSTEREQSLTSCLEKREEMKLEKCVSLPRKESPSVRSSKDGKLLAATLLALLUSCC 60
Qy 45 LTVVSFYQVAALQGDLASRAELQGHAEKLPAGA-----KIFEPPAP 87
Db 61 LTVVSFYQVAALQGDLASRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
Qy 88 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPPWLLSFKRGSALEE 145
Db 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPPWLLSFKRGSALEE 180
Qy 146 -----YGVLYTDTKYANGHLIQRKKVHVFDELSLVTLPFCION----- 185
Db 181 KENKILVKETGYFFIYGVLYTDTKYANGHLIQRKKVHVFDELSLVTLPFCIONMPETL 240
Qy 186 -----LEEGDELQLAIPRENAQISLDGDVTFFGALKLL 218
Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285

RESULT 12
AAE07156
ID AAE07156 standard; Protein; 285 AA.
AC AAE07156;
XX
DT 06-NOV-2001 (first entry)
DE Human tumour necrosis factor (TNF)-delta protein.
DE KW Human; tumour necrosis factor; TNF-delta; gene therapy; antirheumatic;
KW apoptosis; rheumatoid arthritis; cytostatic; sepsis; anti-inflammatory;
KW inflammatory bowel disease; immunosuppressive; antiarthritic; tumour;
KW antibacterial; cancer.
XX
OS Homo sapiens.
XX
PN US2001010925-A1.
XX
PD 02-AUG-2001.
XX
PF 17-NOV-1997; 97US-0971317.
XX
PR 17-NOV-1997; 97US-0971317.
XX
PA (WILEY) WILEY S R.
XX
PI Wiley SR;
XX
DR WPI; 2001-496166/54.
DR N-PSDB; AAD13435.
XX
PT New tumor necrosis factors (TNF)-delta polynucleotide and polypeptide,
PT useful in gene therapy, particularly for treating inflammation, and for
PT inducing apoptosis in cancer and tumor-associated cells to treat cancer
-
XX
PS Claim 16; Page 36-37; 46pp; English.
XX
CC The present sequence is human tumor necrosis factor (TNF)-delta protein.
CC The TNF-delta polynucleotide is useful in gene therapy for modulating
CC TNF-delta. TNF-delta is useful for treating deficiencies of TNF-delta
CC and diseases ameliorated by TNF-delta. TNF-delta is also useful for
CC screening, diagnosing, prognosing, staging or monitoring conditions
CC or diseases attributable to TNF-delta, e.g. inflammation (e.g.
CC inflammatory bowel disease, sepsis or rheumatoid arthritis). The
CC TNF-delta is also useful as an anti-cancer agent to induce apoptosis in
CC cancer and tumour-associated cells.
XX
SQ Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 22; Length 285;
Best Local Similarity 76.5%; Pred. No. 1.1e-103;

```


Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCLEKREEMKKECVSILPRKESPSV-----LLSCC 44
 D 1 MDDSTEREQSLTSCLEKREEMKKECVSILPRKESPSVRSGDKGLAATLLALLSCC 60
 QY 45 LTVVSFYQVAALQGLASLRAELQGHAEKLPAGA-----KIFPPAP 87
 D 61 LTVVSFYQVAALQGLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFPPAP 120
 QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVWLLSFKGSAL-- 145
 D 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVWLLSFKGSAL-- 180
 QY 146 -----YGVLYTDTKYAMGHILQKRVHVFGEDELSTVLFRCIQN----- 185
 D 181 KENKILVKETGYFFIYQVLYTDTKYAMGHILQKRVHVFGEDELSTVLFRCIQNMPETL 240
 QY 186 -----LEGEDELQAIAPRENAQISLDGVDVTFFGALKLL 218
 D 241 PNNSCYSAGIAKLEEGDELQAIAPRENAQISLDGVDVTFFGALKLL 285

RESULT 13

AAE07879 ID AAE07879 standard; Protein; 285 AA.

AAE07879; AC

DT 01-NOV-2001 (first entry)

DE Human BAFF protein.

KW Human; tumour necrosis factor; TNF; APRIL; BAFF; therapy; melanoma;
 KW immune system-related disorder; cancer; renal cell; breast; stomach;
 KW rectal; colon; throat; bladder; ovarian carcinoma; cellular disorder;
 KW gastrointestinal; scleroderma; Kaposi's sarcoma; chronic leukaemia;
 KW squamous cell carcinoma; hyperproliferative condition; pannus formation;
 KW rheumatoid arthritis; postsurgical scarring; fibrosis; liver; uterine;
 KW lung; immunodeficiency; inflammatory disease; lymphadenopathy; vulnary;
 KW autoimmune disease; graft versus host disease; dermatological;
 KW antiinflammatory; immunosuppressive; cytostatic.

OS Homo sapiens.

Key Location/Qualifiers
 Domain 1..46
 /label= Intracellular_domain
 Domain 47..72
 /label= Transmembrane_domain
 Domain 73..285
 /label= Extracellular_domain

XX WO200158949-A2.

XX 16-AUG-2001.

XX 08-FEB-2001; 2001WO-US04121.

XX 11-FEB-2000; 2000US-0181670.

XX (BIOJ) BIOGEN INC.

XX Rennett PD, Thompson JS, Ambrose C, Cachero TG;

XX WPI; 2001-514644/56.

XX N-PSDB; AAD14417.

XX New heteromeric ligand of tumor necrosis factor (TNF) family, useful
 PT for diagnosis, treatment of immune system-related disorders in humans,
 PT comprises TNF-family member APRIL subunit linked non-covalently to
 PT TNF-family member BAFF subunit

PS Claim 2; Fig 2b; 42pp; English.

XX The present invention relates to an isolated heteromeric ligand of
 CC tumour necrosis factor (TNF)-family, referred to as APBF comprising a
 CC TNF-family member APRIL subunit linked non-covalently to TNF-family
 CC member BAFF subunit. APBF is useful for diagnosis or treatment of
 CC various immune system-related disorders in mammals, preferably humans.
 CC Such disorders include cancer, including cellular disorders, for e.g.
 CC renal cell cancer, Kaposi's sarcoma, chronic leukaemia, breast cancer,
 CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma,
 CC colon cancer, bladder cancer, squamous cell carcinoma and
 CC gastrointestinal or stomach cancer, cellular hyperproliferative
 CC conditions, such as scleroderma, pannus formation in rheumatoid
 CC arthritis, postsurgical scarring and lung, liver and uterine fibrosis
 CC and immunodeficiencies, inflammatory diseases, lymphadenopathy,
 CC autoimmune diseases and graft versus host disease. APBF is also useful
 CC for producing monoclonal or polyclonal antibodies and for identifying
 CC novel modulators affecting biological function and receptors interacting
 CC with APBF. The present sequence is human BAFF protein.

XX Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 22; Length 285;

Best Local Similarity 76.5%; Pred. No. 1.1e-103;

Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCLEKREEMKKECVSILPRKESPSV-----LLSCC 44

D 1 MDDSTEREQSLTSCLEKREEMKKECVSILPRKESPSVRSGDKGLAATLLALLSCC 60

QY 45 LTVVSFYQVAALQGLASLRAELQGHAEKLPAGA-----KIFPPAP 87

D 61 LTVVSFYQVAALQGLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFPPAP 120

QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVWLLSFKGSAL-- 145

D 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVWLLSFKGSAL-- 180

QY 146 -----YGVLYTDTKYAMGHILQKRVHVFGEDELSTVLFRCIQN----- 185

D 181 KENKILVKETGYFFIYQVLYTDTKYAMGHILQKRVHVFGEDELSTVLFRCIQNMPETL 240

QY 186 -----LEGEDELQAIAPRENAQISLDGVDVTFFGALKLL 218

D 241 PNNSCYSAGIAKLEEGDELQAIAPRENAQISLDGVDVTFFGALKLL 285

RESULT 14

AAU12183 ID AAU12183 standard; Protein; 285 AA.

XX AAU12183;

XX 24-OCT-2001 (first entry)

XX Human PRO738 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.

XX Homo sapiens.

XX WO200140466-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000WO-US32678.

XX 01-DEC-1999; 99WO-US28301.

XX 01-DEC-1999; 99WO-US28634.

XX 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 PA (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WJ, Zhang Z;
 XX WPI; 2001-408281/43.
 DR N-PSDB; AAS21255.
 XX Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX Claim 12; Fig 24; 813pp; English.
 XX AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PMNCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 SQ Sequence 285 AA;
 Query Match 93.4%; Score 1042.5; DB 22; Length 285;
 Best Local Similarity 76.5%; Pred. No. 1.le-103;
 Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
 QY 1 MDDSTERQSRITSLCKREEMKKECVSILPRKESPSV-----LLSCC 44
 DB 1 MDDSTERQSRITSLCKREEMKKECVSILPRKESPSVRSGKGLLAATYLLALLSCC 60
 QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KTFEPAP 87

Db 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAEPAPAVTAKLIFEPPAP 120
 QY 88 GEGNSSONSNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVFWLLSFKRGSAL-- 145
 Db 121 GEGNSSONSNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVFWLLSFKRGSAL 180
 QY 146 -----YQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLPFCION----- 185
 Db 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLPFCIONMPETL 240
 QY 186 -----LEEGDELOLAIPRENAQISLDGDTFFGALKLL 218
 Db 241 PNNSCYSAGIAKLEEGDELOLAIPRENAQISLDGDTFFGALKLL 285
 RESULT 15
 AAY71915
 ID AAY71915 standard; Protein; 285 AA.
 XX AC AAY71915;
 XX AC AAY71915;
 DT 26-MAR-2001 (first entry)
 XX Human TACI-ligand (TACI-L) protein.
 XX Human; transmembrane activator and CAML interactor; TACI;
 KW tumour necrosis factor receptor; TNF; autoimmune disease; diabetes;
 KW calcium-signal modulating cyclophilin ligand; CAML; viral infection;
 KW neutrokinine alpha polypeptide; TACI-ligand; TACI-L; cytostatic; therapy;
 KW neuroprotective; antidiabetic; antiviral; antinflammatory; tumour;
 KW antiarthritic; antirheumatic; immunosuppressive; multiple sclerosis;
 KW rheumatoid arthritis; graft rejection; inflammation; cell proliferation;
 KW cell death; immunoglobulin E-mediated allergic reaction; Ige.
 XX Homo sapiens.
 OS Homo sapiens.
 FH Key
 FH Domain 1..46
 FT /label= Intracellular_domain
 FT Domain 47..72
 FT /label= Transmembrane_domain
 FT Domain 73..285
 FT /label= Extracellular_domain
 FT Binding-site 123..285
 FT /label= TACI binding site
 FT /note= "Binds with extracellular domain of TACI"
 XX WO200067034-A1.
 PN 09-NOV-2000.
 XX 14-APR-2000; 2000WO-US10282.
 PD 30-APR-1999; 99US-0302863.
 XX (IMMU) IMMUNEX CORP.
 XX Goodwin RG, Din WS;
 XX WPI; 2001-016005/02.
 DR N-PSDB; AAD02007.
 XX Use of new interactions between tumour necrosis factor receptors (TACI)
 PT and TACI ligands to screen candidate molecules for determining agonist
 PT and antagonist interactions which are used for treating inflammation -
 XX Claim 10; Fig 2b; 46pp; English.
 XX The present sequence is a human tumour necrosis factor receptor
 CC (TACI)-ligand (TACI-L) protein.
 CC TACI (Transmembrane activator and calcium-signal modulating
 CC cyclophilin ligand (CAML)-interactor) forms a complex with neutrokinine

CC alpha polypeptide (TACI-Ligand). The antagonist or agonist of
CC TACI/TACI-L complex is useful for modulating an intracellular signalling
CC cascade mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L
CC complex are used to inhibit the interaction between TACI and TACI-L for
CC therapeutic purposes to treat tumour and tumour metastasis and to combat
CC various autoimmune diseases e.g. multiple sclerosis and diabetes, as
CC well as other disorders, such as viral infection, rheumatoid arthritis,
CC graft rejection, and immunoglobulin (Ig) E-mediated allergic reactions
CC and inflammation. The interaction is used to study cellular processes
CC associated with tumour necrosis factor (TNF)-receptors such as immune
CC regulation, cell proliferation, cell death and inflammatory responses.
CC The interaction between the extracellular region of TACI and TACI-L can
CC be used to further develop understanding of which cell types TACI-L
CC acts upon.
XX
SQ Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 22; Length 285;
Best Local Similarity 76.5%; Pred. No. 1.1e-103;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
QY 1 MDDSTEREQSLTCLKKREMKKECVSILPRKESPSV-----LLSCC 44
DB 1 MDDSTEREQSLTCLKKREMKKECVSILPRKESPSV-----LLSCC 60
QY 45 LTVVSFYQVAALQGLASLRRAELQGHAEKLPAGA-----KIPEPPAP 87
DB 61 LTVVSFYQVAALQGLASLRRAELQGHAEKLPAGA-----KIPEPPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTQCLQIADSETPTIQKGYTFVPWLLSPKRGSALE 145
DB 121 GEGNSSQNSRNKRAVQGPETVTQCLQIADSETPTIQKGYTFVPWLLSPKRGSALE 180
QY 146 -----YGOVLYTDKTYAMCHLIQKXHVFGDELSTVLFRCION----- 185
DB 181 KENKILVKETGYFFYIGQVLYTDKTYAMCHLIQKXHVFGDELSTVLFRCIONMPETL 240
QY 186 -----LEEGDELQLAIPRENAQISLDGDVTFPGALKLL 218
DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDVTFPGALKLL 285

Search completed: February 3, 2004, 07:48:16
Job time : 38.3333 secs

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1	1116	100.0	218	9	US-09-911-777-1	Sequence 1, Appli
2	1116	100.0	218	15	US-10-045-574-1	Sequence 1, Appli
3	1042.5	93.4	285	8	US-08-971-317A-2	Sequence 2, Appli
4	1042.5	93.4	285	9	US-09-193-663-2	Sequence 2, Appli
5	1042.5	93.4	285	9	US-09-877-156-1	Sequence 1, Appli
6	1042.5	93.4	285	9	US-09-879-919-3	Sequence 23, Appli
7	1042.5	93.4	285	10	US-09-929-493-2	Sequence 2, Appli
8	1042.5	93.4	285	10	US-09-779-050A-2	Sequence 2, Appli
9	1042.5	93.4	285	11	US-09-302-863-4	Sequence 4, Appli
10	1042.5	93.4	285	11	US-09-880-748-3228	Sequence 3228, Ap
11	1042.5	93.4	285	11	US-09-932-613-173	Sequence 173, Appli
12	1042.5	93.4	285	12	US-10-137-870-24	Sequence 24, Appli
13	1042.5	93.4	285	12	US-10-140-018-24	Sequence 24, Appli
14	1042.5	93.4	285	12	US-10-140-021-24	Sequence 24, Appli
15	1042.5	93.4	285	12	US-10-140-274-24	Sequence 24, Appli

Qy 61 ASLRAELQGHAEKLPAGAKIFEPAPGEGNSSQNRKRAVQGPETVTQDCLQIADS 120
Db 61 ASLRAELQGHAEKLPAGAKIFEPAPGEGNSSQNRKRAVQGPETVTQDCLQIADS 120
Qy 121 ETPTIQKSGYTFVPMWLLSKFGSALYGVLYTDKTYAMGHLIQKRVHVFGEDELSTLTF 180
Db 121 ETPTIQKSGYTFVPMWLLSKFGSALYGVLYTDKTYAMGHLIQKRVHVFGEDELSTLTF 180
Qy 181 RCIONLEEGDELQAIAPRENAQISLDGVTFFGALKLL 218
Db 181 RCIONLEEGDELQAIAPRENAQISLDGVTFFGALKLL 218

RESULT 2

US-10-045-574A-1
; Sequence 1, Application US/10045574A
; Publication No. US20030095967A1
; GENERAL INFORMATION:
; APPLICANT: KALLIED, Susan
; TITLE OF INVENTION: BUFF, Inhibitors Thereof and Their Use
; TITLE OF INVENTION: in the Modulation of B-Cell Response and Treatment of
; FILE REFERENCE: Autoimmune Disorders
; FILE REFERENCE: 08201.0024-01000
; CURRENT APPLICATION NUMBER: US/10/045,574A
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/117,169
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 60/143,228
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: PCR/US00/01788
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/911,777
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PPT
; ORGANISM: Homo Sapien
US-10-045-574A-1

Query Match 100.0%; Score 1116; DB 15; Length 218;
Best Local Similarity 100.0%; Pred. No. 4.4e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVLLSCCLTVVVSFYQVAALQDGL 60
Db 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVLLSCCLTVVVSFYQVAALQDGL 60
Qy 61 ASLRAELQGHAEKLPAGAKIFEPAPGEGNSSQNRKRAVQGPETVTQDCLQIADS 120
Db 61 ASLRAELQGHAEKLPAGAKIFEPAPGEGNSSQNRKRAVQGPETVTQDCLQIADS 120
Qy 121 ETPTIQKSGYTFVPMWLLSKFGSALYGVLYTDKTYAMGHLIQKRVHVFGEDELSTLTF 180
Db 121 ETPTIQKSGYTFVPMWLLSKFGSALYGVLYTDKTYAMGHLIQKRVHVFGEDELSTLTF 180
Qy 181 RCIONLEEGDELQAIAPRENAQISLDGVTFFGALKLL 218
Db 181 RCIONLEEGDELQAIAPRENAQISLDGVTFFGALKLL 218

RESULT 3

US-08-971-317A-2
; Sequence 2, Application US/08971317A
; Publication No. US20010010925A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,317A
; FILING DATE: 17-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goller, Mimi C
; REGISTRATION NUMBER: 39,046
; REFERENCE/DOCKET NUMBER: 6255-US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 935-7550
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20010010925A1e
US-08-971-317A-2

Query Match 93.4%; Score 1042.5; DB 8; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
Qy 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLAATLLALLSCC 60
Qy 45 LTVVSFYQVAALQDGLASLRAELQGHAEKLPAGA-----KIFEPAP 87
Db 61 LTVVSFYQVAALQDGLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
Qy 88 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKSGYTFVPMWLLSKFGSAL-- 145
Db 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKSGYTFVPMWLLSKFGSAL 180
Qy 146 -----YGVLYTDKTYAMGHLIQKRVHVFGEDELSTLTFRCION----- 185
Db 181 KENKILVKETGYFYQVLYTDKTYAMGHLIQKRVHVFGEDELSTLTFRCIONMPETL 240
Qy 186 -----LEEGDELQAIAPRENAQISLDGVTFFGALKLL 218
Db 241 PNNSCYSAGIAKLEEGDELQAIAPRENAQISLDGVTFFGALKLL 285

RESULT 4

US-09-193-663-2
; Sequence 2, Application US/09193663
; Patent No. US20020055624A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255 US.02
; CURRENT APPLICATION NUMBER: US/09/193,663
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/065,916
; EARLIER FILING DATE: 1997-11-17

NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-663-2

Query Match 93.4%; Score 1042.5; DB 9; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKOGKLLAATLLALLSCC 60
QY 45 LTVVSFYQVAALQGDLSRAELQGHAEKLPAGA-----KIFEPAP 87
DB 61 LTVVSFYQVAALQGDLSRAELQGHAEKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSVYTFVPMLLSPKRGSALEE 145
DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSVYTFVPMLLSPKRGSALEE 180
QY 146 -----YGVLYTDTKYAMGHLLIQRKKVHVFGDELSLVTFLFRCIQN 185
DB 181 KENKILVKETGYFFIYGQVLYTDTKYAMGHLLIQRKKVHVFGDELSLVTFLFRCIQNMPETL 240
QY 186 -----LEEGDELQLAIPRENAQISLDGVDVTFPGALKLL 218
DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFPGALKLL 285

RESULT 5

US-09-877-156-1

; Sequence 1, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/877,156
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/286,529
; PRIOR FILING DATE: 1998-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-877-156-1

Query Match 93.4%; Score 1042.5; DB 9; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKOGKLLAATLLALLSCC 60
QY 45 LTVVSFYQVAALQGDLSRAELQGHAEKLPAGA-----KIFEPAP 87
DB 61 LTVVSFYQVAALQGDLSRAELQGHAEKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSVYTFVPMLLSPKRGSALEE 145
DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSVYTFVPMLLSPKRGSALEE 180
QY 146 -----YGVLYTDTKYAMGHLLIQRKKVHVFGDELSLVTFLFRCIQN 185
DB 181 KENKILVKETGYFFIYGQVLYTDTKYAMGHLLIQRKKVHVFGDELSLVTFLFRCIQNMPETL 240

QY 186 -----LEEGDELQLAIPRENAQISLDGVDVTFPGALKLL 218
DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFPGALKLL 285

RESULT 6

US-09-879-919-23

; Sequence 23, Application US/09879919
; Patent No. US20020064829A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-23

Query Match 93.4%; Score 1042.5; DB 9; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKOGKLLAATLLALLSCC 60
QY 45 LTVVSFYQVAALQGDLSRAELQGHAEKLPAGA-----KIFEPAP 87
DB 61 LTVVSFYQVAALQGDLSRAELQGHAEKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSVYTFVPMLLSPKRGSALEE 145
DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSVYTFVPMLLSPKRGSALEE 180
QY 146 -----YGVLYTDTKYAMGHLLIQRKKVHVFGDELSLVTFLFRCIQN 185
DB 181 KENKILVKETGYFFIYGQVLYTDTKYAMGHLLIQRKKVHVFGDELSLVTFLFRCIQNMPETL 240
QY 186 -----LEEGDELQLAIPRENAQISLDGVDVTFPGALKLL 218
DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFPGALKLL 285

RESULT 7

US-09-929-493-2

; Sequence 2, Application US/09929493
; Patent No. US2002011512A1
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Neutrokin-alpha and Neutrokin-alpha Splice Variant
; FILE REFERENCE: PF343P4
; CURRENT APPLICATION NUMBER: US/09/929,493

Query Match 93.4%; Score 1042.5; DB 10; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTDCLQIADSETPTIQKSYTFVPMWLLSFKRGSALEE 145
DB 121 GEGNSSQNSRNKRAVQGPETVTDCLQIADSETPTIQKSYTFVPMWLLSFKRGSALEE 180
QY 146 -----YQVLYTDKTYAMGHLIQKRVHVFQDELSTLFRCIQN----- 185
DB 181 KENKILVKETGYFFIYQVLYTDKTYAMGHLIQKRVHVFQDELSTLFRCIQNMPETL 240
QY 186 -----LLEGDELQALAI PRENAQISLDGDTFFFGALKLL 218
DB 241 PNNCSYAGIAKLEEGDELQALAI PRENAQISLDGDTFFFGALKLL 285
RESULT 9
US-09-929-493-2
; Sequence 4, Application US/09302863
; Publication No. US2003002233A1
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; APPLICANT: Din, Wanwan S
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/302,863
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-929-493-2

Query Match 93.4%; Score 1042.5; DB 10; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTDCLQIADSETPTIQKSYTFVPMWLLSFKRGSALEE 145
DB 121 GEGNSSQNSRNKRAVQGPETVTDCLQIADSETPTIQKSYTFVPMWLLSFKRGSALEE 180
QY 146 -----YQVLYTDKTYAMGHLIQKRVHVFQDELSTLFRCIQN----- 185
DB 181 KENKILVKETGYFFIYQVLYTDKTYAMGHLIQKRVHVFQDELSTLFRCIQNMPETL 240
QY 186 -----LLEGDELQALAI PRENAQISLDGDTFFFGALKLL 218
DB 241 PNNCSYAGIAKLEEGDELQALAI PRENAQISLDGDTFFFGALKLL 285
RESULT 8
US-09-779-050A-2
; Sequence 2, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, WILLIAM
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-2

Query Match 93.4%; Score 1042.5; DB 10; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTDCLQIADSETPTIQKSYTFVPMWLLSFKRGSALEE 145
DB 121 GEGNSSQNSRNKRAVQGPETVTDCLQIADSETPTIQKSYTFVPMWLLSFKRGSALEE 180
QY 146 -----YQVLYTDKTYAMGHLIQKRVHVFQDELSTLFRCIQN----- 185
DB 181 KENKILVKETGYFFIYQVLYTDKTYAMGHLIQKRVHVFQDELSTLFRCIQNMPETL 240
QY 186 -----LLEGDELQALAI PRENAQISLDGDTFFFGALKLL 218
DB 241 PNNCSYAGIAKLEEGDELQALAI PRENAQISLDGDTFFFGALKLL 285
RESULT 9
US-09-302-863-4
; Sequence 4, Application US/09302863
; Publication No. US2003002233A1
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; APPLICANT: Din, Wanwan S
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/302,863
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Human
US-09-302-863-4

Query Match 93.4%; Score 1042.5; DB 11; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 60
QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTDCLQIADSETPTIQKSYTFVPMWLLSFKRGSALEE 145
DB 121 GEGNSSQNSRNKRAVQGPETVTDCLQIADSETPTIQKSYTFVPMWLLSFKRGSALEE 180
QY 146 -----YQVLYTDKTYAMGHLIQKRVHVFQDELSTLFRCIQN----- 185
DB 181 KENKILVKETGYFFIYQVLYTDKTYAMGHLIQKRVHVFQDELSTLFRCIQNMPETL 240
QY 186 -----LLEGDELQALAI PRENAQISLDGDTFFFGALKLL 218
DB 241 PNNCSYAGIAKLEEGDELQALAI PRENAQISLDGDTFFFGALKLL 285
RESULT 10
US-09-880-748-3228
; Sequence 3228, Application US/09880748
; Publication No. US20030059937A1

GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3228
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3228

Query Match 93.4%; Score 1042.5; DB 11; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
QY 45 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGA-----KIFEPPAP 87
Db 61 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
QY 88 GEGNSSQNSNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 145
Db 121 GEGNSSQNSNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
QY 146 -----YGVLYTDKTYAMGHLIQKRVHVFQDGLSLVTLFRCIQN----- 185
Db 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLIQKRVHVFQDGLSLVTLFRCIQNMPETL 240
QY 186 -----LEEGDELQALAI PRENAQISLDGVDVTFPGALKLL 218
Db 241 PNNSCYSAGIAKLEEGDELQALAI PRENAQISLDGVDVTFPGALKLL 285

RESULT 11
US-09-932-613-173
; Sequence 173, Application US/0932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 173
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-932-613-173

Query Match 93.4%; Score 1042.5; DB 11; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;

Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
QY 45 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGA-----KIFEPPAP 87
Db 61 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
QY 88 GEGNSSQNSNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 145
Db 121 GEGNSSQNSNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
QY 146 -----YGVLYTDKTYAMGHLIQKRVHVFQDGLSLVTLFRCIQN----- 185
Db 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLIQKRVHVFQDGLSLVTLFRCIQNMPETL 240
QY 186 -----LEEGDELQALAI PRENAQISLDGVDVTFPGALKLL 218
Db 241 PNNSCYSAGIAKLEEGDELQALAI PRENAQISLDGVDVTFPGALKLL 285

RESULT 12
US-10-137-870-24
; Sequence 24, Application US/10137870
; Publication No. US20030138883A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvarcoff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C155
; CURRENT APPLICATION NUMBER: US/10/137,870
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 24
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-870-24

Query Match 93.4%; Score 1042.5; DB 12; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
QY 45 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGA-----KIFEPPAP 87
Db 61 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
QY 88 GEGNSSQNSNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 145
Db 121 GEGNSSQNSNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy 146 -----YGOVLYTDKTYAMGHILQKRVHFGDELSTLTLFRCIQN----- 185
Db 181 KENKILVKETGYFFIYGOVLYTDKTYAMGHILQKRVHFGDELSTLTLFRCIQNMPETL 240
Qy 186 -----LBEDELQLAIPRENAQISLDGVDVTFFGALKLL 218
Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285

RESULT 13

US-10-140-018-24

; Sequence 24, Application US/10140018

; Publication No. US20030138885A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C158

; CURRENT APPLICATION NUMBER: US/10/140,018

; CURRENT FILING DATE: 2002-05-06

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 24

; LENGTH: 285

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-140-018-24

Query Match 93.4%; Score 1042.5; DB 12; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

Qy 3 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
Qy 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPAP 87
Db 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAPAGKAGLEAPAVTAGLKIFEPAP 120

Qy 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSFKRGSALEE 145
Db 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSFKRGSALEE 180
Qy 146 -----YGOVLYTDKTYAMGHILQKRVHFGDELSTLTLFRCIQN----- 185
Db 181 KENKILVKETGYFFIYGOVLYTDKTYAMGHILQKRVHFGDELSTLTLFRCIQNMPETL 240
Qy 186 -----LBEDELQLAIPRENAQISLDGVDVTFFGALKLL 218
Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285

RESULT 14

US-10-140-021-24

; Sequence 24, Application US/10140021

; Publication No. US20030138886A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C167
; CURRENT APPLICATION NUMBER: US/10/140,021
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 24
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-021-24

Query Match 93.4%; Score 1042.5; DB 12; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

Qy 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
Qy 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPAP 87
Db 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAPAGKAGLEAPAVTAGLKIFEPAP 120
Qy 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSFKRGSALEE 145
Db 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSFKRGSALEE 180
Qy 146 -----YGOVLYTDKTYAMGHILQKRVHFGDELSTLTLFRCIQN----- 185
Db 181 KENKILVKETGYFFIYGOVLYTDKTYAMGHILQKRVHFGDELSTLTLFRCIQNMPETL 240
Qy 186 -----LBEDELQLAIPRENAQISLDGVDVTFFGALKLL 218
Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285

RESULT 15

US-10-140-274-24

; Sequence 24, Application US/10140274

; Publication No. US20030143674A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C161
; CURRENT APPLICATION NUMBER: US/10/140,274
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 24
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-274-24

Query Match 93.4%; Score 1042.5; DB 12; Length 285;
Best Local Similarity 76.5%; Pred. No. 7, 7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
Qy 1 MDDSTEREQSRLTSCCLKREMKLKECVSILPRKESPSV-----LSSCC 44
Db 1 MDDSTEREQSRLTSCCLKREMKLKECVSILPRKESPSVRSSKDGKLLAATLLALLSSCC 60
Qy 45 LTVVSFYQVAALQGLASLRAELQGHAEKLPAG-----KIFEPAP 87
Db 61 LTVVSFYQVAALQGLASLRAELQGHAEKLPAGAPVAGLKIPEPPAP 120
Qy 88 GEGNSSQNRNKRVAQGPETVTQCLQLIADSETPTIQKSYTFVPWLLSFKRGSAL-- 145
Db 121 GEGNSSQNRNKRVAQGPETVTQCLQLIADSETPTIQKSYTFVPWLLSFKRGSAL 180
Qy 146 -----YQVLYTDKTYAMGHILQKRVHVFQDELSTLFRICION----- 185
Db 181 KENKILVKETGYFFTYGQVLYTDKTYAMGHILQKRVHVFQDELSTLFRICIONPETL 240
Qy 186 -----LEEGDELQLAIPRENAQISLDGDTFFGALKLL 218
Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285

Search completed: February 3, 2004, 08:02:16
Job time : 212.218 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 3, 2004, 07:43:37 ; Search time 14.0489 Seconds
(without alignments)
656.548 Million cell updates/sec

Title: US-09-911-777-1

Perfect score: 1116

Sequence: 1 MDDSTEREQSLTSLCKRE.....ENAIQLDGDVTFPGALKLL 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/aaa/5B COMB.pap:*
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- 6: /cgn2_6/ptodata/1/aaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1042.5	93.4	285	3	US-09-286-529-1
2	1042.5	93.4	285	4	US-09-589-287B-2
3	1042.5	93.4	285	4	US-09-496-118B-1
4	1042.5	93.4	285	4	US-09-565-423-2
5	1042.5	93.4	285	4	US-09-879-919-23
6	1042.5	93.4	285	4	US-09-588-947A-2
7	927	83.1	266	4	US-09-589-287B-19
8	927	83.1	266	4	US-09-879-919-24
9	927	83.1	266	4	US-09-588-947A-19
10	779.5	69.8	219	4	US-09-589-287B-28
11	779.5	69.8	219	4	US-09-588-947A-28
12	773.5	69.3	219	4	US-09-589-287B-30
13	773.5	69.3	219	4	US-09-588-947A-30
14	681	61.0	174	4	US-09-496-118B-5
15	533	47.8	145	3	US-09-286-529-21
16	523.5	46.9	289	4	US-09-589-287B-38
17	523.5	46.9	289	4	US-09-588-947A-38
18	379	34.0	155	4	US-09-589-287B-23
19	379	34.0	155	4	US-09-588-947A-23
20	196	17.6	46	4	US-09-496-118B-2
21	152	13.6	250	3	US-08-883-086-2
22	151	13.5	205	3	US-09-565-423-3
23	151	13.5	205	3	US-09-286-529-5
24	150	13.4	233	4	US-10-082-260-2
25	150	13.4	233	4	US-08-815-783-2
26	150	13.4	233	4	US-09-879-919-2
27	150	13.4	250	3	US-09-153-927-4

28	150	13.4	250	4	US-09-879-919-11	Sequence 11, Appl
29	144	12.9	234	4	US-09-157-864-2	Sequence 2, Appl
30	144	12.9	247	4	US-09-157-864-4	Sequence 4, Appl
31	142	12.7	234	4	US-09-879-919-13	Sequence 13, Appl
32	134	12.0	168	4	US-10-082-260-4	Sequence 4, Appl
33	134	12.0	168	4	US-08-815-783-4	Sequence 4, Appl
34	134	12.0	168	4	US-09-879-919-4	Sequence 4, Appl
35	126.5	11.3	147	3	US-08-883-086-3	Sequence 3, Appl
36	123	11.0	136	4	US-09-589-287B-20	Sequence 20, Appl
37	123	11.0	136	4	US-09-947A-20	Sequence 20, Appl
38	110	9.9	31	4	US-09-496-118B-3	Sequence 3, Appl
39	92.5	8.3	34	4	US-09-496-118B-4	Sequence 4, Appl
40	83.5	7.5	630	4	US-09-300-909-20	Sequence 20, Appl
41	83	7.4	384	4	US-09-648-004-6	Sequence 6, Appl
42	81.5	7.3	737	4	US-09-772-647-4	Sequence 4, Appl
43	80	7.2	261	3	US-08-961-083-164	Sequence 164, App
44	80	7.2	261	4	US-09-536-784-164	Sequence 164, App
45	78	7.0	281	3	US-09-118-408-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-286-529-1
; Sequence 1, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286.529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-286-529-1

Query Match 93.4%; Score 1042.5; DB 3; Length 285;
Best Local Similarity 76.5%; Pred. No. 5.4e-118;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY	1	MDDSTEREQSLTSLCKREMKLKECVSIIPRKESPSV-----LLSCC 44
DB	1	MDDSTEREQSLTSLCKREMKLKECVSIIPRKESPSVRSKQKGLLAATLLALLSCC 60
QY	45	LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
DB	61	LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
QY	88	CEGSSQNSRNRKRAVQGPETVTQCLQIADSETPTIQGSIYTFVPWLLSFKRGSL-- 145
DB	121	CEGSSQNSRNRKRAVQGPETVTQCLQIADSETPTIQGSIYTFVPWLLSFKRGSALEE 180
QY	146	-----YGOVLYTDKTYAMGHILQKRVHVFQDELSTLFRCIQ----- 185
DB	181	KENKILVKETGYFTYGOVLYTDKTYAMGHILQKRVHVFQDELSTLFRCIQMPETL 240
QY	186	-----LEEGDLSQLAIIPRENAQISLDGDVTFPGALKLL 218
DB	241	PNNCSYAGIAKLREGDELQAIIPRENAQISLDGDVTFPGALKLL 285

RESULT 2

US-09-589-287B-2
; Sequence 2, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha

Query Match 93.4%; Score 1042.5; DB 4; Length 285;
Best Local Similarity 76.5%; Pred. No. 5.4e-118;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4

Query Match 93.4%; Score 1042.5; DB 4; Length 285;
Best Local Similarity 76.5%; Pred. No. 5.4e-118;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4

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; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-23

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Query Match          93.4%; Score 1042.5; DB 4; Length 285;
Best Local Similarity 76.5%; Pred. No. 5.4e-118;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVSSKDGKLLAATLLALLSCC 60
QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
Db 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAPKAGLEAPAVTAGLKIFEPPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKSYTFVPWLLSFKRGSAL-- 145
Db 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKSYTFVPWLLSFKRGSAL 180
QY 146 -----YGVLYTDKTYAMGHLLQKRVHVFQDELSTLFRICQN----- 185
Db 181 KENKILVKETGYFFYGVLYTDKTYAMGHLLQKRVHVFQDELSTLFRICQNMPETL 240
QY 186 -----LEEGDELQLAIPRENAQISLDGVDVTFPGALKLL 218
Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFPGALKLL 285

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RESULT 6

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US-09-588-947A-2
; Sequence 2, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C2
; CURRENT APPLICATION NUMBER: US/09/588,947A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/130,696
; PRIOR FILING DATE: 1999-04-23

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; PRIOR APPLICATION NUMBER: 60/131,278
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131,673
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/136,784
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,659
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: 60/145,824
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 60/167,239
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 60/168,624
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: PCV/US96/17957
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-588-947A-2

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Query Match          93.4%; Score 1042.5; DB 4; Length 285;
Best Local Similarity 76.5%; Pred. No. 5.4e-118;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVSSKDGKLLAATLLALLSCC 60
QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
Db 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAPKAGLEAPAVTAGLKIFEPPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKSYTFVPWLLSFKRGSAL-- 145
Db 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKSYTFVPWLLSFKRGSAL 180
QY 146 -----YGVLYTDKTYAMGHLLQKRVHVFQDELSTLFRICQN----- 185
Db 181 KENKILVKETGYFFYGVLYTDKTYAMGHLLQKRVHVFQDELSTLFRICQNMPETL 240
QY 186 -----LEEGDELQLAIPRENAQISLDGVDVTFPGALKLL 218
Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFPGALKLL 285

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RESULT 7

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US-09-589-287B-19
; Sequence 19, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-19

Query Match      83.1%; Score 927; DB 4; Length 266;
Best Local Similarity 69.8%; Pred. No. 5e-104;
Matches 199; Conservative 0; Mismatches 0; Indels 86; Gaps 5;

QY 1 MDDSTEREOSRLTSCCLKREEMKLEKCVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREOSRLTSCCLKREEMKLEKCVSILPRKESPSVRSKDGKGLAATLLALLSCC 60
QY 45 LTVVSFYQVAALOGDLASLRAELQGHAEKLPAGA-----KIFEPAP 87
Db 61 LTVVSFYQVAALOGDLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKGYTFVFWLLSPKRGSALEE 145
Db 121 GEGNSSQNSRNKRAVQGPET-----GSYTFVFWLLSPKRGSALEE 161
QY 146 -----YQGVLYTDKTYAMGHLIQRKQVHVFGDELSLVTFLFRCIQN 185
Db 162 KENKILVKETGYFFIYQGVLYTDKTYAMGHLIQRKQVHVFGDELSLVTFLFRCIQNMPETL 221
QY 186 -----LESGDELOLAIPRENAQISLDGVDVTFFGALKLL 218
Db 222 PNNCSYAGIAKLESGDELOLAIPRENAQISLDGVDVTFFGALKLL 266

RESULT 8
US-09-879-919-24
; Sequence 24, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-24

Query Match      83.1%; Score 927; DB 4; Length 266;
Best Local Similarity 69.8%; Pred. No. 5e-104;
Matches 199; Conservative 0; Mismatches 0; Indels 86; Gaps 5;

QY 1 MDDSTEREOSRLTSCCLKREEMKLEKCVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREOSRLTSCCLKREEMKLEKCVSILPRKESPSVRSKDGKGLAATLLALLSCC 60
QY 45 LTVVSFYQVAALOGDLASLRAELQGHAEKLPAGA-----KIFEPAP 87
Db 61 LTVVSFYQVAALOGDLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKGYTFVFWLLSPKRGSALEE 145
Db 121 GEGNSSQNSRNKRAVQGPET-----GSYTFVFWLLSPKRGSALEE 161
QY 146 -----YQGVLYTDKTYAMGHLIQRKQVHVFGDELSLVTFLFRCIQN 185
Db 162 KENKILVKETGYFFIYQGVLYTDKTYAMGHLIQRKQVHVFGDELSLVTFLFRCIQNMPETL 221
QY 186 -----LESGDELOLAIPRENAQISLDGVDVTFFGALKLL 218
Db 222 PNNCSYAGIAKLESGDELOLAIPRENAQISLDGVDVTFFGALKLL 266

RESULT 9
US-09-588-947A-19
; Sequence 19, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C2
; CURRENT APPLICATION NUMBER: US/09/588,947A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/130,696
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 60/131,278
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131,673
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/136,784
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,659
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: 60/145,824
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 60/167,239
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 60/168,624
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: PCT/US96/17957
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 42
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Qy 146 -----YQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLPFCION----- 185
Db 121 VKETGYFFIYQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLPFCIONMPETLPNNSCY 180
Qy 186 -----LEEGDELOLAIPRENAQISLDGDTFFGALKLL 218
Db 181 SAGIAKLEEGDELOLAIPRENAQISLDGDTFFGALKLL 219

RESULT 12
US-09-589-287B-30
; Sequence 30, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-30

Query Match 69.3%; Score 773.5; DB 4; Length 219;
Best Local Similarity 73.5%; Pred. No. 1.6e-85;
Matches 161; Conservative 3; Mismatches 4; Indels 51; Gaps 3;

Qy 51 YQVAALQGDLSLRAELQGHAEKLP-----AGAKIFEPAPGEGNSS 93
Db 1 YQVAAVQGDLSLRAELQGHAEKLPARAPAKAGLGEAPAVTAGLKIFEPAPGEGNSS 60
Qy 94 QNSNRKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSL----- 145
Db 61 QSSNRKRAIQAEETVIQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKIL 120
Qy 146 -----YQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLPFCION----- 185
Db 121 VKETGYFFIYQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLPFCIONMPETLPNNSCY 180
Qy 186 -----LEEGDELOLAIPRENAQISLDGDTFFGALKLL 218
Db 181 SAGIAKLEEGDELOLAIPRENAQISLDGDTFFGALKLL 219

RESULT 13
US-09-588-947A-30
; Sequence 30, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; CURRENT APPLICATION NUMBER: US/09/588,947A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16

Qy 146 -----YQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLPFCION----- 185
Db 121 VKETGYFFIYQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLPFCIONMPETLPNNSCY 180
Qy 186 -----LEEGDELOLAIPRENAQISLDGDTFFGALKLL 218
Db 181 SAGIAKLEEGDELOLAIPRENAQISLDGDTFFGALKLL 219

RESULT 14
US-09-496-118B-5
; Sequence 5, Application US/09496118B
; Patent No. 6475986
; GENERAL INFORMATION:
; APPLICANT: Aggarwal, Bharat B.
; TITLE OF INVENTION: Uses of THANK, a TNF homologue that Activates
; TITLE OF INVENTION: Apoptosis
; FILE REFERENCE: D6206
; CURRENT APPLICATION NUMBER: US/09/496,118B
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: US 60/118,531
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 13
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Qy 146 -----YQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLPFCION----- 185
Db 121 VKETGYFFIYQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLPFCIONMPETLPNNSCY 180
Qy 186 -----LEEGDELOLAIPRENAQISLDGDTFFGALKLL 218
Db 181 SAGIAKLEEGDELOLAIPRENAQISLDGDTFFGALKLL 219

RESULT 14
US-09-496-118B-5
; Sequence 5, Application US/09496118B
; Patent No. 6475986
; GENERAL INFORMATION:
; APPLICANT: Aggarwal, Bharat B.
; TITLE OF INVENTION: Uses of THANK, a TNF homologue that Activates
; TITLE OF INVENTION: Apoptosis
; FILE REFERENCE: D6206
; CURRENT APPLICATION NUMBER: US/09/496,118B
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: US 60/118,531
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 13
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Qy 146 -----YQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLPFCION----- 185
Db 121 VKETGYFFIYQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLPFCIONMPETLPNNSCY 180
Qy 186 -----LEEGDELOLAIPRENAQISLDGDTFFGALKLL 218
Db 181 SAGIAKLEEGDELOLAIPRENAQISLDGDTFFGALKLL 219

RESULT 14
US-09-496-118B-5
; Sequence 5, Application US/09496118B
; Patent No. 6475986
; GENERAL INFORMATION:
; APPLICANT: Aggarwal, Bharat B.
; TITLE OF INVENTION: Uses of THANK, a TNF homologue that Activates
; TITLE OF INVENTION: Apoptosis
; FILE REFERENCE: D6206
; CURRENT APPLICATION NUMBER: US/09/496,118B
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: US 60/118,531
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 13
```

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; SEQ ID NO 5
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: domain
; LOCATION: 112..285
; OTHER INFORMATION: sequence of THANK extracellular domain
US-09-496-118B-5

Query Match          61.0%; Score 681; DB 4; Length 174;
Best Local Similarity 80.3%; Pred. No. 1.9e-74;
Matches 139; Conservative 0; Mismatches 0; Indels 34; Gaps 2;

QY 80 KIFEPPAPCEGNSQNSRNRKRAVQPEETVTQDCLQLIADSETPTIQGSYTFVPWLLSF 139
Db 2 KIFEPPAPCEGNSQNSRNRKRAVQPEETVTQDCLQLIADSETPTIQGSYTFVPWLLSF 61

QY 140 KRGSAL-----YGVLYTDKTYAMGHILQKRVHVFGEDELSLVTLPFC 182
Db 62 KRGSALKEENKILVKETGYFFIYGVLYTDKTYAMGHILQKRVHVFGEDELSLVTLPFC 121

QY 183 ION-----LEEGDELAIPRENAQISLDGDTFFFGALKLL 218
Db 122 IQNMPETLPNNSCYSAGIAKLEEGDELAIPRENAQISLDGDTFFFGALKLL 174
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RESULT 15
US-09-286-529-21
; Sequence 21, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-286-529-21
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Query Match          47.8%; Score 533; DB 3; Length 145;
Best Local Similarity 76.6%; Pred. No. 1.3e-56;
Matches 111; Conservative 0; Mismatches 0; Indels 34; Gaps 2;

QY 108 TVTQDCLQLIADSETPTIQGSYTFVPWLLSFKRGSA-----YGVYL 150
Db 1 TVTQDCLQLIADSETPTIQGSYTFVPWLLSFKRGSALEENKILVKETGYFFIYGVYL 60

QY 151 YTDKTYAMGHILQKRVHVFGEDELSLVTLPFCION-----LEEGDELA 193
Db 61 YTDKTYAMGHILQKRVHVFGEDELSLVTLPFCIONMPETLPNNSCYSAGIAKLEEGDELA 120

QY 194 LAIPRENAQISLDGDTFFFGALKLL 218
Db 121 LAIPRENAQISLDGDTFFFGALKLL 145
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Search completed: February 3, 2004, 07:44:54
Job time : 16.0489 secs

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Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	85	7.1	767	2	I51083	SOX-LZ - rainbow t
2	84.5	7.0	380	2	A70646	probable PPE prote
3	82.5	6.9	1153	2	T26883	hypothetical prote
4	81.5	6.8	1121	1	C87973	protein V43FEC.12
5	81	6.7	449	1	A38449	regulatory protein
6	81	6.7	891	2	T25714	hypothetical prote
7	80.5	6.7	1735	2	A57607	Munc13-1 - rat
8	80	6.6	613	2	S27770	hypothetical prote
9	80	6.6	842	2	T41697	translation elonga
10	79.5	6.6	573	2	B70732	probable secD - My
11	78.5	6.5	313	2	H96303	alpha-galactoside
12	78.5	6.5	498	1	VGBGX	secreted glycoprot
13	78.5	6.5	737	2	S72442	actin-fragmin kina
14	78.5	6.5	1015	2	C84918	probable ATP-depen
15	78.5	6.5	15281	2	S41309	cyclosporin synth
16	78	6.5	373	2	A79426	flagellar P-ring p
17	78	6.5	373	2	A12643	flagellar P-ring p
18	78	6.5	391	2	C84268	aspartate aminotra
19	77.5	6.4	383	1	VGBXKG	glycoprotein presu
20	77.5	6.4	404	2	B83466	hypothetical prote
21	77.5	6.4	434	2	T20400	hypothetical prote
22	77.5	6.4	454	2	A56954	yes-associated pro
23	77.5	6.4	920	2	C96831	hypothetical prote
24	77	6.4	2359	2	AH3009	non-ribosomal pept
25	77	6.4	2399	2	F98274	hypothetical prote
26	77	6.4	3005	1	GNWSTV	genome polyprotein
27	76.5	6.4	218	2	A96831	hypothetical prote
28	76.5	6.4	882	2	T43250	spindle pole body
29	76.5	6.4	1070	2	T05733	kinasin homolog F2


```

A:Molecule type: mRNA
A:Residues: 1-1735 <RES>
A:Cross-references: EMBL;U24070; NID:g915327; PIDN:AAC52266.1; PID:g915328
C:Superfamily: protein kinase C zinc-binding repeat homology
F:567-616/Domain: protein kinase C zinc-binding repeat homology <K22>

Query Match      6.7%; Score 80.5; DB 2; Length 1735;
Best Local Similarity 23.3%; Pred. No. 85;
Matches 47; Conservative 26; Mismatches 58; Indels 71; Gaps 12;

Qy 19 KGED-MKVGVDPIIPQK--EEGAVL--LSSFTAM-----SLYQLAALQADIMLRME 66
      |||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 858 KGBDAMKVVYDE-TAGEIVDEFAMRYGVESIYQAMTHFACLSKMYCPCGPVAVMSTLLAN 916
      |||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 67 LQSYRGSGATPAA-----AKLLTPAAPRPHNSR-----GHNRRAPFG 104
      :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 917 INAYYAHHTASTNVNSASDRPAASFNGKRPVKLL-----DQLNSLRIDLSMYRNNPASS 972
      :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 105 PETEQDV-----DLSAPPALRNIIOCLQLIADSDPTTKRGTYTF 146
      |||:|||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 973 PERL-QDLKSTVDLLTSTIIFFRMKVQELQSPPRASQVVKDCVACLNS-----TYEY 1023
      |||:|||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 147 VPWLLSFKRGNALYSQVLYTDP 168
      :||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1024 I-----FNNCHLEYGREYOTDP 1040
      :||:||||:||||:||||:||||:||||:||||:||||:||||:

```

```

RESULT 8
S27770
hypothetical protein 1 - African malaria mosquito (fragment)
C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
C;Accession: S27770
R;Besansky, N.J.; Paskewitz, S.M.; Mills-Hamm, D.M.; Collins, F.H.
submitted to the EMBL Data Library, June 1992
A;Description: Distinct families of site-specific retroposons occupy identical
A;Reference number: S27770
A;Accession: S27770
A;Molecule type: DNA
A;Residues: 1-613 <BES>
A;Cross-references: EMBL:M93690; NID:g159615; PID:g159616

Query Match          6.6%; Score 80; DB 2; Length 613;
Best Local Similarity 29.2%; Pred. No. 25;
Matches 35; Conservative 16; Mismatches 37; Indels 32; Gaps 6;

QY 17 SERGEDMKV-----GYDPTTPQKEGAVLLSSSFTAMSLYQLA-----AL 56

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Db      109   :SQRREEMTVPATSTPPKAGKCSSAEPSPSENMNESKLK-----AMQVAQLSKSLCKREL 163
Qy      57   QADLMN---LRMELQVYRGSAIPAAAKLLTPAAPRPHNSRG---HNRNRAFPGPPETEQ 110
Db      164   QESLKNVAALERELETYRMGAR-SVIELOQQAAAAAPMTTAQGAHSRRNRGRGPGPQQEQ 222

RESULT 9
T41697
translation elongation factor eEF-2 [similarity] - fission yeast (Schizosacchar
C:Species: Schizosaccharomyces pombe
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C/Accession: T41897; T39256; T38896; T51993; T51994; T42427/
R/Wedler, H.; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A/Reference number: Z22010
A/Accession: T41697
A/Molecule type: DNA
A/Residues: 1-842 <WED>
A/Cross-references: EMBL:AL118159; PIDN:CA958373.1; GSPDB:GNO0068; SPDB:SPCP31B
A/Experimental source: strain 972H-; clone p1 p31510
A/Genetics: SP2
R/Stevens, K.; Churcher, C.; McDougall, R.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, August 1999
A/Reference number: Z21838
A/Reference number: Z21838

A;Residues: 1-737 <EIC1>

A:Reference-number: S45487; MUID:95094306; PMID:8001164

A;Residues: 1-737 <EIC1>

A:Accession: S45487
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-15281 <WEB>
A:Cross-references: EMBL:Z28383; NID:G440168; PIDN:CAA82227.1; PID:G440169
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
A>Note: only a part of the translation is shown
A>Note: the source is designated as Tolypocladium inflatum
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: cyclosporin fungus cyclosporin synthetase; acetate-CoA ligase homology; a
C:Keywords: carrier protein; phosphopantetheine; phosphoprotein
F:532-1008/Domain: acetate-CoA ligase homology <ACLI>
F:1029-1096/Domain: acyl carrier protein homology <ACP1>
F:1618-2069/Domain: acetate-CoA ligase homology <ACL2>
F:2527-2594/Domain: acyl carrier protein homology <ACP2>
F:3115-3553/Domain: acetate-CoA ligase homology <ACL3>
F:4014-4081/Domain: acyl carrier protein homology <ACP3>
F:4601-5057/Domain: acetate-CoA ligase homology <ACL4>
F:5506-5573/Domain: acyl carrier protein homology <ACP4>
F:6094-6546/Domain: acetate-CoA ligase homology <ACL5>
F:7003-7070/Domain: acyl carrier protein homology <ACP5>
F:7591-8042/Domain: acetate-CoA ligase homology <ACL6>
F:8063-8130/Domain: acyl carrier protein homology <ACP6>
F:8652-9157/Domain: acetate-CoA ligase homology <ACL7>
F:9558-9625/Domain: acyl carrier protein homology <ACP7>
F:10146-10586/Domain: acetate-CoA ligase homology <ACL8>
F:11055-11122/Domain: acyl carrier protein homology <ACP8>
F:11635-12106/Domain: acetate-CoA ligase homology <ACL9>
F:12127-12194/Domain: acyl carrier protein homology <ACP9>
F:12715-13159/Domain: acetate-CoA ligase homology <ACL10>
F:13623-13690/Domain: acyl carrier protein homology <ACP10>
F:14213-14676/Domain: acetate-CoA ligase homology <ACL11>
F:14698-14765/Domain: acyl carrier protein homology <ACP11>
F:1060,2558,4045,5537,7034,8094,9589,11086,12158,13654,14729/Binding site: phosphopanted

Query Match 6.5%; Score 78.5; DB 2; Length 15281;
Best Local Similarity 24.8%; Pred. No. 2e+03; 55; Indels 73; Gaps 12;
Matches 50; Conservative 24; Mismatches 55; Indels 73; Gaps 12;
QY 37 GAVLLSSFTAMSLYQLAALQADLMRLME--LQSYRG-SATPAAAKLLTPAAPRPHNSS 93
Db 3592 GHVLEVGITGTVLP-----NLGREGGLQSYGVGLSPSPSATAFVNKAA----- 3634
QY 94 RCHRNRRAPCPPEE-----TEQDV-----DLSAPPALRNII-----QDCL-QLIADS 134
Db 3635 -----KSPFGLGDRIRVEVGATDIDRLGDLHAGLVVNSVAQYFPSPQDYLAQLVRD- 3687
QY 135 DPTIRKGTFTVPWLLSPKGNALYSOVLYTDPFAMGHVQIQR-----KKVHVFGEDELS 189
Db 3688 -----LTKVPGV-----ERIFFGD---MRSHAINRDFLVARAVHALGDKAT 3725
QY 190 LVTLFRFCIONLEEGDEIQLAIP 211
Db 3726 KAEIQREVVVRMESEDELLVDP 3747

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Job time : 17.4356 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
Run on: February 3, 2004, 07:43:37 ; Search time 9.79556 Seconds
(without alignments)
1113.790 Million cell updates/sec
Title: US-09-911-777-2
Perfect score: 1204
Sequence: 1 MDESATLPPCLFCSEK.....ENAIQRNGDDTFGALKL 232
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 127863 segs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result #	No.	Score	Match	Query %	ID	Description
1	1103.5	91.7	309	1	T13B_MOUSE	Q9w72 mus musculus
2	622.5	51.7	285	1	T13B_HUMAN	Q9y275 homo sapien
3	151	12.5	241	1	TN13_MOUSE	Q9d777 mus musculus
4	149	12.4	250	1	TN13_HUMAN	O75888 homo sapien
5	83	6.9	410	1	AUP1_MOUSE	P70295 mus musculus
6	81	6.7	449	1	ALGB_PSEAE	P23747 pseudomonas
7	80	6.6	842	1	EP2_SCHPO	O14460 schizosacch
8	79.5	6.6	428	1	HISX_LACPL	P59399 lactobacill
9	79.5	6.6	573	1	SECD_MYCTU	Q50634 mycobacteri
10	79.5	6.6	2167	1	SHK1_RAT	Q9wv48 rattus norv
11	79	6.6	513	1	TI60_HUMAN	Q92993 homo sapien
12	78.5	6.5	498	1	VGLX_PVRVI	P07562 pseudorabie
13	78	6.5	373	1	FLGI_AGRTS	Q44340 agrobacteri
14	77.5	6.4	383	1	VGLZ_HSVK	P32515 equine herp
15	77.5	6.4	454	1	YAP1_HUMAN	P46937 homo sapien
16	77	6.4	732	1	TRPE_AZOB	P50872 azospirillu
17	77	6.4	923	1	HXK3_HUMAN	P52790 zea mays
18	77	6.4	3023	1	POLG_TVMV	P09814 t genome po
19	76.5	6.4	882	1	DIS1_SCHPO	Q09933 schizosacch
20	76.5	6.4	1755	1	PEPL_MOUSE	Q9r269 mus musculu
21	76	6.3	1403	1	NID2_MOUSE	O88322 mus musculu
22	75.5	6.3	297	1	YPHB_BACSU	P50742 bacillus su
23	75.5	6.3	346	1	TRPA_WAIZE	P42390 zea mays (m
24	75.5	6.3	735	1	IF2C_GUITH	O78489 guillardia
25	75.5	6.3	1210	1	BAT8_HUMAN	Q96Kq7 homo sapien
26	75	6.2	430	1	ORC2_CAEEL	Q21037 caenorhabdi
27	74.5	6.2	357	1	MYCM_HUMAN	P12525 homo sapien
28	74.5	6.2	428	1	YQP1_CAEEL	O09302 caenorhabdi
29	74.5	6.2	448	1	YAP1_CHICK	P46936 gallus gall
30	74	6.1	789	1	PRTP_EBV	P25939 Epstein-Bar
31	74	6.1	797	1	VGLX_HSVB	P28968 equine herp
32	74	6.1	1147	1	SRE1_HUMAN	P36956 homo sapien
33	73.5	6.1	472	1	YFHD_ECOLI	P30135 escherichia

RESULT 1				
T13B_MOUSE				
ID	T13B_MOUSE	STANDARD;	PRT;	309_AA.
AC	Q9WU72;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 13B (B cell-activating factor) (BAFF).			
DE	TNFSF13B OR BAFF.			
GN	Mus musculus (Mouse).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9288033; PubMed=10359578;			
RA	Schneider P., Mackay F., Steiner V., Hofmann K., Bodmer J.-L.,			
RA	Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,			
RA	Valmori D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L.,			
RA	Tschopp J.;			
RT	"BAFF", a novel ligand of the tumor necrosis factor family, stimulates			
RT	B cell growth.";			
RL	J. Exp. Med. 189:1747-1756 (1999).			
RN	[2]			
RC	SEQUENCE FROM N.A., AND VARIANT SER-79.			
RC	STRAIN=NZB;			
RX	MEDLINE=21850530; PubMed=11862414;			
RA	Jiang Y., Ohtsui M., Abe M., Li N., Xiu Y., Wen X.S., Shirai T.,			
RA	Hirose S.;			
RT	"Polymorphism and chromosomal mapping of the mouse gene for B-cell			
RT	activating factor belonging to the tumor necrosis factor family			
RT	(Baff) and association with the autoimmune phenotype.";			
RL	Immunogenetics 53:810-813 (2001).			
CC	-1- FUNCTION: Cytokine that binds to TNFSF13B/TACI and TNFSF17/BCMA.			
CC	TNFSF13/APRIL binds to the same 2 receptors. Together, they form a			
CC	2 ligands - 2 receptors pathway involved in the stimulation of B-			
CC	and T-cell function and the regulation of humoral immunity. A			
CC	third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the			
CC	survival of mature B-cells and the B-cell response.			
CC	-1- SUBUNIT: Homotrimer.			
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN			
CC	EXTRACELLULAR SOLUBLE FORM.			
CC	-1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY			
CC	PROTEOLYTIC PROCESSING.			
CC	-1- SIMILARITY: Belongs to the tumor necrosis factor family.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF119383; AAD22475.1; -.			

Q9zra4 deinococcus
Q9zje9 helicobacte
Q9wvj0 mus musculu
O89047 rattus norv
Q9y566 homo sapien
O30409 b tyrocidin
Q89ah0 macaca mula
O84771 chlamydia t
O67728 aquifex aeo
Q04841 mus musculu
P07313 oryctolagus

ALIGNMENTS

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DR EMBL; AF352245; AAL83939.1; -.
DR MGD; MGI:1344376; Tnfef13b.
DR InterPro; IPR006052; TNF_family.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE NEG.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor;
KW Polymorphism.
FT CHAIN 1 309 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT CHAIN 127 309 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT CHAIN 127 309 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT DOMAIN 1 47 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 48 68 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 69 309 EXTRACELLULAR (POTENTIAL).
FT SITE 126 127 CLEAVAGE (BY SIMILARITY).
FT DISULFID 256 269 BY SIMILARITY.
FT CARBOHYD 117 117 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 79 N -> S (IN STRAIN NZB).
SQ SEQUENCE 309 AA; 34192 MW; F3DE6056866034B4 CRC64;
Query Match 91.7%; Score 1103.5; DB 1; Length 309;
R Best Local Similarity 74.4%; Pred. No. 2e-96;
R Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;
QY 1 MDESATLPPPCLCFCSEKGEKMGKGYDPTTPQKEGA-----VLLSS 43
DB 1 MDESATLPPPCLCFCSEKGEKMGKGYDPTTPQKEGA-----VLLSS 60
QY 44 SFTAMSLVQLAALQADLMLNLMELQSYRGSATPAAA-----KLTPAAPRPHNSR 94
DB 61 SFTAMSLVQLAALQADLMLNLMELQSYRGSATPAAAAGAPELTAGVKLTTPAAPRPHNSR 120
QY 95 GHRNRRAPFGPETEQDVLSDAPPA-----LRNIQDCLQLIADSDTP 137
DB 121 GHRNRRAPFGPETEQDVLSDAPPAAPCLPGCRHSQDDNGMNLNIIQDCLQLIADSDTP 180
QY 138 TIRKGTITYFVPWLLSFKEGNAL-----YSQVLYTDDIFANGHVIQRKK 180
DB 181 TIRKGTITYFVPWLLSFKEGNALKEKENKIVVRQGTGYFFIYSQVLYTDDIFANGHVIQRKK 240
QY 181 VHVFGDELVLTLFRICION-----LEEGDBIQLAIPRENAQISRGDD 223
DB 241 VHVFGDELVLTLFRICIONMPTLNNSCYSNGIARLEBGEIQLAIPRENAQISRGDD 300
QY 224 TFFGALKLL 232
DB 301 TFFGALKLL 309
RESULT 2
T13B HUMAN STANDARD; PRT; 285 AA.
AC Q9V275;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 13B (TNF and APOL-
DE related leukocyte expressed ligand 1) (TALL-1) (B lymphocyte
DE stimulator) (BLYS) (B cell-activating factor) (BAFF) (Dendritic cell-
DE derived TNF-like molecule).
GN TNFSF13B OR TALL1 OR BLYS OR BAFF OR ZTNF4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99260341; PubMed=10331498;
RA Shu H.-B., Hu W.-H., Johnson H.;
RT "TALL-1 is a novel member of the TNF family that is down-regulated by

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RT mitogens";
RN J. Leukoc. Biol. 65:680-683(1999).
RL [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 134-148.
RX MEDLINE=99288033; PubMed=10359578;
RA Schneider P., Mackay P., Steiner V., Hofmann K., Bodmer J.-L.,
RA Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,
RA Valmoril D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L.,
RA Tschopp J.;
RT "BAFF, a novel ligand of the tumor necrosis factor family, stimulates
RT B cell growth.";
RN J. Exp. Med. 189:1747-1756(1999).
RL [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Monocytes, and Neutrophils;
RA MEDLINE=99323343; PubMed=10398604;
RA Moore P.A., Belvedere O., Orr A., Pieri K., Lafleur D.W., Feng P.,
RA Soppet D., Charters M., Gentz R., Parmelee D., Li Y., Gaiparina O.,
RA Giri J., Roschke V., Nardelli B., Carrell J., Sosnovtseva S.,
RA Greenfield W., Ruben S.M., Olsen H.S., Fikes J., Hilbert D.M.;
RT "Blys: member of the tumor necrosis factor family and B lymphocyte
RT stimulator.";
RN Science 285:260-263(1999).
RL [4]
RP SEQUENCE FROM N.A.
RX Farrah T., Gross J., Piddington C., O'Hara P.;
RA "Homo sapiens homolog of tumor necrosis factor.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Dendritic cell;
RA Zhang W., Wan T., Yu Y., Cao X.;
RT "A novel dendritic cell-derived TNF-like molecule.";
RN Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RL [6]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RA MEDLINE=22388257; PubMed=12477932;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner I., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [7]
RP SEQUENCE OF 1-135 FROM N.A., AND VARIANT THR-105.
RX Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
RA "New polymorphisms of human Blys gene.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [8]
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TNFRI: system for regulating
RT humoral immunity.";
RN Nat. Immunol. 1:252-256(2000).
RL [9]

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RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 142-285.
 RX MEDLINE=21842897; PubMed=11853672;
 RA Liu Y., Xu L., Opalka N., Kappler J., Shu H.-B., Zhang G.;
 RT "Crystal structure of sTALL-1 reveals a virus-like assembly of TNF
 family ligands."; <http://www.isb-sib.ch/announcement/>
 RL Cell 108:383-394(2002).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 136-285.
 RX MEDLINE=21686304; PubMed=11827482;
 RA Karpusas M., Cachero T.G., Qian F., Borlack-Sjodin A., Mullen C.,
 RA Strauch K., Hsu Y.-M., Kallied S.L.;
 RT "Crystal structure of extracellular human BAFF, a TNF family member
 that stimulates B lymphocytes."; <http://www.isb-sib.ch/announcement/>
 RL J. Mol. Biol. 315:1145-1154(2002).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 134-285.
 RX MEDLINE=21912420; PubMed=11862220;
 RA Oren D.A., Li Y., Volovik Y., Morris T.S., Dharla C., Das K.,
 RA Galperina O., Gentz R., Arnold E.;
 RT "Structural basis of BLYS receptor recognition."; <http://www.isb-sib.ch/announcement/>
 RL Nat. Struct. Biol. 9:288-292(2002).
 CC -!- FUNCTION: Cytokine that binds to TNFSF13B/TACI and TNFSF17/BCMA.
 CC TNFSF13/APRIL binds to the same 2 receptors. Together, they form a
 CC 2 ligands - 2 receptors pathway involved in the stimulation of B-
 CC and T-cell function and the regulation of humoral immunity. A
 CC third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the
 CC survival of mature B-cells and the B-cell response.
 CC -!- SUBUNIT: Homotrimer.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 CC EXTRACELLULAR SOLUBLE FORM.
 CC -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN PERIPHERAL BLOOD
 CC LEUKOCYTES AND IS SPECIFICALLY EXPRESSED IN MONOCYTES AND
 CC MACROPHAGES. ALSO FOUND IN THE SPLEEN, LYMPH NODE, BONE MARROW, T-
 CC CELLS AND DENDRITIC CELLS. A LOWER EXPRESSION SEEN IN PLACENTA,
 CC HEART, LUNG, FETAL LIVER, THYMUS, AND PANCREAS.
 CC -!- INDUCTION: UPREGULATED BY EXPOSURE TO INTERFERON-GAMMA. DOWN-
 CC REGULATED BY PHORBOL MYRISTATE ACETATE/IONOMYCIN TREATMENT.
 CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
 CC PROTEOLYTIC PROCESSING.
 CC -!- PTM: N-glycosylated.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 DR EMBL; AF136293; AAD29421.1; -;
 DR EMBL; AF136456; AAD35356.1; -;
 DR EMBL; AF132600; AAD21092.1; -;
 DR EMBL; AF136114; AAF01432.1; -;
 DR EMBL; AF134715; AAF60219.1; -;
 DR EMBL; AB073225; BAB90856.1; -;
 DR EMBL; BC020674; AAB20674.1; -;
 DR PDB; 1KXG; 03-APR-02.
 DR PDB; 1KD7; 12-NOV-02.
 DR PDB; 1JH5; 08-FEB-02.
 DR Genew; HGNC:11929; TNFSF13B.
 DR MIM; 603969; -;
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR006052; TNF_family.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; FALSE_NEG.
 DR PROSITE; PS00499; TNF_2; 1.
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure;
 KW Polymorphism.
 FT CHAIN 1 285 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY

FT CHAIN 134 285 MEMBER 13B, MEMBRANE FORM.
 FT FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT FT MEMBER 13B, SOLUBLE FORM.
 FT FT CYTOPLASMIC (POTENTIAL).
 FT FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT FT (POTENTIAL).
 FT FT EXTRACELLULAR (POTENTIAL).
 FT FT CLEAVAGE.
 FT FT N-LINKED (GLCNAC. . .).
 FT FT N-LINKED (GLCNAC. . .) (HIGH MANNOSE).
 FT FT A -> T.
 FT FT /FTID=VAR_013483.
 FT STRAND 146 151
 FT TURN 153 154
 FT STRAND 158 160
 FT TURN 161 162
 FT STRAND 163 165
 FT STRAND 168 174
 FT STRAND 178 181
 FT TURN 182 183
 FT STRAND 184 187
 FT STRAND 191 201
 FT STRAND 208 215
 FT TURN 221 222
 FT STRAND 226 234
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 FT TURN 266 267
 FT STRAND 270 270
 FT TURN 274 276
 FT STRAND 278 283
 SQ SEQUENCE 285 AA; 31222 MW; 48ED0D7AB38C8867 CRC64;
 Query Match 51.7%; Score 622.5; DB 1; Length 285;
 Best Local Similarity 48.7%; Pred. No. 3.3e-51;
 Matches 146; Conservative 23; Mismatches 48; Indels 83; Gaps 7;
 QY 1 MDESAKTLPPPLCLFCSEKEDMKV-GYDPTTPPOKEGAV-----LSS 43
 DB 1 MDDSTER-EGSRLTSCLLKREEMKLCVSLPRKESPSVRSKDGKLLAATLLALLSC 59
 QY 44 SFTAMSLYQLAALQADLMNLRMELQSYRGSGATPAA-----KLLTPAA 86
 DB 60 CLTVSVYQVALQGLDASLAELOGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEP 119
 QY 87 PRPHNSRGHRNRRAFPPEPEQDVLSDAPPALRNIIQDCLQIADSDTPIRGVTTF 146
 DB 120 PEGNSNSQNSRKAQVQPEET-----VTQDCLQIADSETPTIQGSYTF 165
 QY 147 VPWLLSPKRGNA-----YSQVLYTDPFAMGHVIOKKVHVFGDELS 189
 DB 166 VPWLLSPKRGSALEKENKILVETGYFFIYGVQVLYTDPFAMGHVIOKKVHVFGDELS 225
 QY 190 LVTLFRCIQN-----LEEGDEIQLAIPRENAQISRGDDTFFGALKLL 232
 DB 226 LVTLFRCIQNMPETLPNNNSCYSGIAKLEEGDEIQLAIPRENAQISLGDVTFFGALKLL 285
 RESULT 3
 TN13 MOUSE
 ID TN13 MOUSE STANDARD; PRT; 241 AA.
 AC Q9D777; Q9ERP1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 13 (A proliferation-
 DE inducing ligand) (APRIL).
 GN TNFSF13 OR APRIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Sciurognathia; Muridae; Murinae; Mus.
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=21170294; PubMed=10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
 RA "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
 RT humoral immunity."; 252-256(2000).
 RL Nat. Immunol. 1:252-256(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glasi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 RL
 CC -!- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and to
 CC TNFRSF17/BCMA. May be implicated in the regulation of tumor cell
 CC growth. May be involved in monocyte/macrophage-mediated
 CC immunological processes.
 CC
 CC -!- SUBUNIT: Homotrimer (Potential).
 CC
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing.
 CC
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 CC
 CC
 DR EMBL; AF294825; AAG22534.1; -;
 DR EMBL; AK009514; BAB26332.1; -;
 DR MGD; MGI:1916833; Tnfsl3.
 DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
 DR InterPro; IPR006052; TNF_family.
 DR Pfam; PF00229; TNF; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF 1; 1.
 DR PROSITE; PS0049; TNF 2; 1.
 KW Cytokine; Immune response; Glycoprotein.
 FT PROPEP 1 95
 FT CHAIN 96 241
 FT
 FT SITE 95 96
 FT DISULFID 187 202
 FT CARBOHYD 115 115
 FT CONFLICT 120 120
 SQ SEQUENCE 241 AA; 26889 MW; 4B96D03BDC712A4 CRC64;
 Query Match 12.5%; Score 151; DB 1; Length 241;

Best Local Similarity 26.9%; Pred. No. 6.1e-07;
 Matches 66; Conservative 24; Mismatches 75; Indels 80; Gaps 9;
 QY 37 GAVLLSSSFAMSLYQLAQLADLMLRMELQSYRGSAATPAAAKLLTPAARPHNS----- 92
 DB 27 GAVLGAVTCAVALLIQ-----QTELOSRLRREVSRLQSGSPSQKQ-----GSRPWQSLWEQ 77
 QY 93 -----SRGHRNRRAFPGPETEODVDLSAPPALRNIIQDCLQIADSDTPTIRKG 142
 DB 78 SPDVLEAWKDKAKSRERRAVLTQKHKHSHVLPV--NITSK-----ADSDV----- 124
 QY 143 TYTFVPMWLLSPKRGNA-----LYSQVLYTDPIFAMGHVTRKKVHVFG 185
 DB 125 --TEVMWQPVLRRCRGLEAQGDIVRVMDTGILYLSQVLFHDVTFVTMGQVYSRE----- 176
 QY 186 DELSLVTLFRCIQ-----NLEEGDEIQLAIPRENAQISRNQDDPTFF 226
 DB 177 GQGRRETFLRCIRSMPSDPPRAYNSCYSAGVFHLHQGDITVKIPRANAKLSLSPHGFTL 236
 QY 227 GALKL 231
 DB 237 GFVKL 241
 RESULT 4
 TN13 HUMAN STANDARD; PRT; 250 AA.
 ID TN13 HUMAN STANDARD; PRT; 250 AA.
 AC O75888; Q96HV6; Q9PIM8; Q9PIM9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 13 (A proliferation-
 DE inducing ligand) (APRIL) (TNF- and ABOL-related leukocyte expressed
 DE ligand 2) (TALL-2) (TNF-related death ligand-1) (TRDL-1).
 GN TNFSF13 OR APRIL OR TALL2 OR ZTNF2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RX MEDLINE=98416181; PubMed=9743536;
 RA Hahne M., Kataoka T., Schroeter M., Hofmann K., Imler M.,
 RA Bodmer J.-L., Schneider P., Bornand T., Holler N., French L.E.,
 RA Sordat B., Rimoldi D., Tschopp J.;
 RT "APRIL, a new ligand of the tumor necrosis factor family, stimulates
 RT tumor cell growth.";
 RL J. Exp. Med. 188:1185-1190(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99260341; PubMed=10331498;
 RA Shu H.-B., Hu W.-H., Johnson H.;
 RT "TALL-1 is a novel member of the TNF family that is down-regulated by
 RT mitogens.";
 RL J. Leukoc. Biol. 65:680-683(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Farrah T., Grant F., Haldeman B., Whitmore T., Gross J., O'Hara P.;
 RT "Homo sapiens tumor necrosis factor homolog.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).
 RX MEDLINE=20168636; PubMed=10706119;
 RA Kelly K.A., Manos E.J., Jensen G.T., Nadauld L., Jones D.A.;
 RT "APRIL/TRDL-1, a tumor necrosis factor-like ligand, stimulates cell
 RT death.";
 RL Cancer Res. 60:1021-1027(2000).
 RN [5]
 RP SEQUENCE OF 1-247 FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Heu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity.";
RL Nat. Immunol. 1:252-256 (2000).
RN [7]
RP PROCESSING BY FURIN, MUTAGENESIS OF ARG-101 AND ARG-104, AND
RP SUBCELLULAR LOCATION.
RX MEDLINE=21486098; PubMed=11571266;
RA Lopez-Fraga M., Fernandez R., Albar J.P., Hahne M.;
RT "Biologically active APRIL is secreted following intracellular
RT processing in the Golgi apparatus by furin convertase.";
RL EMBO Rep. 2:945-951 (2001).
CC -!- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and to
CC TNFRSF17/BCMA. May be implicated in the regulation of tumor cell
CC growth. May be involved in monocyte/macrophage-mediated
CC immunological processes.
CC -!- SUBUNIT: Homotrimer (Potential).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=Alpha;
CC IsoId=O75888-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=O75888-2; Sequence=VSP_006450;
CC Name=Gamma;
CC IsoId=O75888-3; Sequence=VSP_006451;
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN TRANSFORMED CELL
CC LINES, CANCERS OF COLON, THYROID, LYMPHOID TISSUES AND
CC SPECIFICALLY EXPRESSED IN MONOCYTES AND MACROPHAGES.
CC -!- INDUCTION: DOWN-REGULATED BY PHORBOL MYRISTATE ACETATE/IONOMYCIN
CC TREATMENT.
CC -!- PTM: The precursor is cleaved by furin.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF046888; AAC61312.1; -
CC EMBL; AF136294; AAD29422.1; -
CC EMBL; AF184972; AAF01321.1; -
CC EMBL; AF114011; AAF59828.1; -
CC EMBL; AF114012; AAF59829.1; -
CC EMBL; AF114013; AAF59830.1; -
CC EMBL; BC008042; AAH08042.1; -

DR Genew; HGNC:11928; TNFSF13.
DR MIM; 604472; -
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR006052; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS00049; TNF 2; 1.
KW Cytokine; Immune response; Glycoprotein;
KW Alternative splicing.
FT PROPEP 1 104
FT CHAIN 105 250
FT SITE 104 105 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT DISULFID 196 211 MEMBER 13.
FT CARBOHYD 124 124 CLEAVAGE (BY FURIN).
FT VARSPLIC 113 129 POTENTIAL.
FT VARSPLIC 247 249 N-LINKED (GLCNAC..) (POTENTIAL).
FT MUTAGEN 101 104 KOHSLVHLVFNATSKD -> N (in isoform Beta).
FT CONFLICT 96 96 /FTID=VSP_006450.
FT CONFLICT 247 247 Missing (in isoform Gamma).
SQ SEQUENCE 250 AA; 27433 MW; AEA6B9457F6E298 CRC64;
Query Match 12.4%; Score 149; DB 1; Length 250;
Best Local Similarity 25.9%; Pred. No. 9.9e-07;
Matches 58; Conservative 27; Mismatches 73; Indels 66; Gaps 7;
QY 53 LAALQADLMRLMELQSVKSGATPAAXALLTPAAPRPNSS-----RGHRNRAPP 103
DB 48 LITQTELOSLRREVSRLQGTGGPQNGEGVWQSLPQSSDALAEWNGERSRRRAVL 107
QY 104 GPEETEQDVLSAPPALRNIIQDCLQLIADSDTPTIRKGTVTFFVWLLSFKRGNA----- 158
DB 108 TQKQKQKSHLVHLVFNATSKD-----DSDV-----TEVMQPALRRGRGLQAQG 152
QY 159 -----LYSQVLYTDPFAMGHVIOKRVKVVHFGDELVLTLPRCIO----- 198
DB 153 YGVRIQDAGVYLLVSVLFDVPTFTMGQVSVRE-----GQGRQETLPRCIRMPSPDR 206
QY 199 -----NLEGDGIQALIPRENAQISRGNDTFFGAKL 231
DB 207 AYNCSYAGVPHLHQGDILSVIIPARAKLNLSPHGTFLGFVKL 250
RESULT 5
AUP1_MOUSE
ID AUP1_MOUSE STANDARD; PRT; 410 AA.
AC P70295;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ancient ubiquitous protein 1 precursor.
GN AUP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=96411699; PubMed=8812468;
RA Jang W., Weber J.S., Bashir R., Bushby K., Meisler M.H.;
RT "Aup1, a novel gene on mouse chromosome 6 and human chromosome 2p13.";
RL Genomics 36:366-368 (1996).
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: BELONGS TO THE AUP1 FAMILY.
CC -----
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EMBL; U41736; AAC52839.1; -;
MGD; MGI:107789; Aupl.
InterPro; IPR002123; Acyltransferase.
InterPro; IPR003892; CUB.
Pfam; PF02845; CUB; 1.
SMART; SM00546; CUB; 1.
SMART; SM00563; PLsC; 1.
Signal.
CHAIN 1 37 POTENTIAL.
38 410 ANCIENT UBQUITOUS PROTEIN 1.
SEQUENCE 410 AA; 46121 MW; E7D070CEB296B5B CRC64;

Query Match 6.9%; Score 83; DB 1; Length 410;
Best Local Similarity 22.1%; Pred. No. 3.1;
Matches 44; Conservative 20; Mismatches 77; Indels 58; Gaps 7;

4 SAKTLPPLCPFCSEKEDMKVG-----YDPTPKKEGAV----- 39
148 STRLPPTLLPPEEATNGREGLRFSSWPFISQDVVQPLTLQVRPLSVTVSDASWV 207
40 --LLSSSTANSLYOLAALQADLMRLMELQSYRGSSATPAAK-----LLTPAARPH 90
208 SELLWSLFPVFTYQVRLPIRQLGSEEFALRVQOLVAKELGIGTRITLPADKAH 267
91 NSSRGHNR-----APGPBETQDVDLA-----PPALRNIIQ-----DCLQ 129
268 MKRQRPRLRPOSVOSSPSPSPSDVLTTLAHRVKEVLPVPLNVIQRLARTGCV 327
130 LIADSDTPTIRKGTTFVP 148
328 LTITN-----LLEGAVAFNP 342

RESULT 6
ID ALGB_PSEAE STANDARD; PRT; 449 AA.
AC P23747;
DT 01-NOV-1991 (Rel. 20, Created)
HT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alginate biosynthesis transcriptional regulatory protein algb.
OS ALGB OR PA5483.
GN Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate FRD;
RX MEDLINE=91139582; PubMed=1899859;
RA Wozniak D.J., Ohman D.E.;
RT "Pseudomonas aeruginosa Algb, a two-component response regulator of the NtrC family, is required for algd transcription."
RL J. Bacteriol. 173:1406-1413 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92149314; PubMed=1738315;
RA Goldberg J.B., Danke T.;
RT "Pseudomonas aeruginosa Algb, which modulates the expression of alginates, is a member of the NtrC subclass of prokaryotic regulators."
RL Mol. Microbiol. 6:59-66 (1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."
RL Nature 406:959-964 (2000).
CC -!- FUNCTION: POSITIVE REGULATOR OF ALGINATE BIOSYNTHETIC GENE (ALGD).
CC -!- SIMILARITY: Contains 1 response regulatory domain.
CC -!- SIMILARITY: Contains 1 sigma-54 factor interaction ATP-binding domain.

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EMBL; M62902; AAA25700.1; -;
EMBL; M82823; -; NOT ANNOTATED CDS.
EMBL; AE004961; AAG0868.1; -;
PIR; A38449; A38449.
HSSP; P41789; 1NTR.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR002197; HTH_Pis.
InterPro; IPR001789; Response_reg.
InterPro; IPR002078; Sig54_interact.
Pfam; PF02954; HTH_8; 1.
Pfam; PF00072; response_reg; 1.
Pfam; PF00158; Sigma54_activat; 1.
ProDom; PD000039; Response_reg; 1.
SMART; SM00382; AAA; 1.
SMART; SM00448; REC; 1.
TIGRfams; TIGR01199; HTH_fis; 1.
PROSITE; PS01110; RESPONSE REGULATORY; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; 1.
PROSITE; PS00676; SIGMA54_INTERACT_2; 1.
PROSITE; PS00688; SIGMA54_INTERACT_3; 1.
PROSITE; PS00045; SIGMA54_INTERACT_4; 1.
KW Sensory transduction; Phosphorylation; Transcription regulation; DNA-binding; Activator; ATP-binding; Alginate biosynthesis; Complete proteome.
KW DOMAIN 10 124 RESPONSE REGULATORY.
FT MOD_RES 59 59 PHOSPHORYLATION (BY SIMILARITY).
FT DOMAIN 147 376 SIGMA-54 FACTOR INTERACTION (POTENTIAL).
FT NP_BIND 175 182 ATP (POTENTIAL).
FT NP_BIND 238 247 ATP (POTENTIAL).
FT DN_BIND 426 445 H-T-H MOTIF (BY SIMILARITY).
SQ SEQUENCE 449 AA; 49323 MW; E6452B88457CBC17 CRC64;

Query Match 6.7%; Score 81; DB 1; Length 449;
Best Local Similarity 25.7%; Pred. No. 5.3;
Matches 37; Conservative 18; Mismatches 63; Indels 26; Gaps 6;

7 TLPPCLPCFCSEKEDMKVGYPIT-----PQEEGAVLLSSSTAMSLYOLAAL 56
254 TLQPKLLRFIQDK-EYERVG-DPVTTRADVRLAATNRDLGAMVAQQGFREDLLRLNVI 311
57 QADLMRLMELQSYRGSSATPAAKLLTP-AAPRPHNSRGHNRRAFPGPETEODVLS 115
312 VLNPPLPPEEADILGLAERFLARFVKDYGPRGPFSEAREAMKQYWPVGNVRE----- 366
116 APPALRNIIQD-----CQLIADSD 135
367 ----LRNVIERASIIICQELVDVD 386

RESULT 7
EF2_SCHPO STANDARD; PRT; 842 AA.
ID EF2_SCHPO

AC 014460; Q9USG7; Q9US29; Q9UT64;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Elongation factor 2 (EF-2).
 GN (EFT1 OR SPCP1B10.07) AND (EFT2 OR SPACS13.01C OR SPAPYU71.04C).
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JY333;
 RX MEDLINE=97254480; PubMed=9098980;
 RA Mita K., Morimyo M., Ito K., Sugaya K., Ebihara K., Hongo E.,
 RA Higashi T., Hirayama Y., Nakamura Y.,
 RT "Comprehensive cloning of Schizosaccharomycetes pombe genes encoding
 RT translation elongation factors.";
 RL Gene 187:259-266(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (EFT1 AND EFT2).
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornaby T., Howarth S., Huckle E.J., Hunt S., Jegels K.,
 RA James K., Jones L., Jones M., Leacher S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Foreburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakowski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomycetes pombe.";
 RL Nature 415:871-880(2002).
 CC -!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLLOCATION
 CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
 CC RIBOSOME (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
 CC EF-G/EF-2 SUBFAMILY.
 CC
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 CC
 CC EMBL; D83976; BA23591.1;
 CC EMBL; D83975; BA23590.1;
 CC EMBL; AL121859; CAB58373.1;
 CC EMBL; AL122032; CAB58724.1;
 CC EMBL; AL109734; CAB52147.1;
 CC FIR; T41697; T41697.
 CC GeneDB_Spombe; SPACS13.01c;
 CC GeneDB_Spombe; SPCP1B10.07;

DR InterPro; IPR000795; EF_GTPbind.
 DR InterPro; IPR000640; EFG_C.
 DR InterPro; IPR005517; EFG_IV.
 DR InterPro; IPR004161; EFTU_D2.
 DR InterPro; IPR005225; Small_GTP.
 DR Pfam; PF00679; EFG_C; 1.
 DR Pfam; PF03764; EFG_IV; 1.
 DR Pfam; PF00009; GTP_EFTU; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 1.
 DR PRINTS; PR00315; ELONGATNFCT.
 DR TIGRFam; TIGR00231; small_GTP; 1.
 DR PROSITE; PS00301; EFATOR_GTP; 1.
 KW Elongation factor; Protein biosynthesis; GTP-binding.
 FT NP_BIND 26 33 GTP (BY SIMILARITY).
 FT NP_BIND 104 108 GTP (BY SIMILARITY).
 FT NP_BIND 158 161 GTP (BY SIMILARITY).
 FT MOD_RES 699 699 DIPHTHAMIDE (BY SIMILARITY).
 FT CONFLICT 821 823 EAR -> DVG (IN REF. 1).
 SQ SEQUENCE 842 AA; 93230 MW; A544C5C454BC55C7 CRC64;
 Query Match 6.6%; Score 80; DB 1; Length 842;
 Best Local Similarity 20.2%; Pred. No. 15;
 Matches 53; Conservative 28; Mismatches 76; Indels 106; Gaps 12;
 QY 11 PC-ICFCSEKEDMKVGYDPTPOKEEGAVLLSSFTAMSLYQLAALQADLNLRLMLQ- 68
 DB 516 PCVLCTTSSEGEHIVAG-----AGELHLEIC-----LKDLOEDHAGIPLKISP 558
 QY 69 ---SVRSATPAAKLLTPAAPRHNS-----SEGHENRR----- 100
 DB 559 PWSYRESVSEPSMTALSKSPKHNRIFTMTAEMSELSVAIETGHVNPDRDDFKVRARI 618
 QY 101 -----APPGPEETEQD---VDLSAPPALRNIIQD----- 126
 DB 619 MADEFGHVDVTDARKWCF-GDPTTCANVVVDQTKAVYLNIKSVVAAPAWASKEGPMF 677
 QY 127 -----CLQIADSDTPIRKGTFTFVPLLSFKRGNALYSQVLYTDPIF----- 170
 DB 678 EENLSCRFNILDVVLHAD--AIHGGGQIIPTRRVVYASTLLASPIQEPVFLVEIQV 735
 QY 171 ---AMG---HVIOQRKHVFGDE 187
 DB 736 SENAMGGIYSVINKRGHVFSEE 758
 RESULT 8
 HISX_LACPL
 ID HISX_LACPL STANDARD; PRT; 428 AA.
 AC P59399;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Histidinol dehydrogenase (EC 1.1.1.23) (HDH).
 GN HISD OR LP 2559.
 OS Lactobacillus plantarum.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIMB 8826 / WCFS1;
 RX MEDLINE=22480296; PubMed=12566566;
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
 RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
 RA Hofer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
 RA De Vos W.M., Siezen R.J.;
 RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
 CC -!- FUNCTION: Catalyzes the sequential NAD-dependent oxidations of L-
 CC histidinol to L-histidinolaldehyde and then to L-histidine (By
 CC similarity).
 CC -!- CATALYTIC ACTIVITY: L-histidinol + 2 NAD(+) + H(2)O = L-histidine

DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE SH3 and multiple ankyrin repeat domains protein 1 (Shank1) (GKAP/SAPAP
 DE interacting protein) (SPANK-1) (Synamon) (Somatostatin receptor
 DE interacting protein) (SSTR interacting protein) (SSTRIP).
 GN SHANK1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 3), AND INTERACTION WITH DLGAP1 AND
 DLG4.
 RP TISSUE=Brain;
 RC MEDLINE=99419021; PubMed=10488079;
 RA Yao I., Hata Y., Hixson K., Deguchi M., Ide N., Takeuchi M., Takai Y.;
 RT "Synamon, a novel neuronal protein interacting with synapse-associated
 RT protein 90/postsynaptic density-95-associated protein.";
 RL J. Biol. Chem. 274:27463-27466(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 4), AND INTERACTION WITH DLGAP1.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=99360850; PubMed=10433268;
 RA Naisbitt S., Kim E., Tu J.C., Xiao B., Sala C., Valtchanoff J.,
 RT Weinberg R.J., Worley P.F., Sheng M.;
 RT "Shank, a novel family of postsynaptic density proteins that binds to
 RT the NMDA receptor/PSD-95/GKAP complex and cortactin.";
 RL Neuron 23:569-582(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=20549637; PubMed=10958799;
 RA Tobaben S., Suedhof T.C., Stahl B.;
 RT "The G protein-coupled receptor C11 interacts directly with proteins
 RT of the Shank family.";
 RL J. Biol. Chem. 275:36204-36210(2000).
 RN [4]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5), AND
 RP DEVELOPMENTAL STAGE.
 RC TISSUE=Brain;
 RX MEDLINE=99436166; PubMed=10506216;
 RA Lim S., Naisbitt S., Yoon J., Hwang J.I., Suh P.G., Sheng M., Kim E.;
 RT "Characterization of the Shank family of synaptic proteins. Multiple
 RT genes, alternative splicing, and differential expression in brain and
 RT development.";
 RL J. Biol. Chem. 274:29510-29518(1999).
 RN [5]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM 4).
 RC TISSUE=Brain;
 RX MEDLINE=20020275; PubMed=10551867;
 RA Zitzer H., Hoenck H.-H., Baechner D., Richter D., Kreienkamp H.-J.;
 RT "Somatostatin receptor interacting protein defines a novel family of
 RT multidomain proteins present in human and rodent brain.";
 RL J. Biol. Chem. 274:32997-33001(1999).
 RN [6]
 RP INTERACTION WITH HOMER-1, AND SUBCELLULAR LOCATION.
 RX MEDLINE=99360651; PubMed=10433269;
 RA Tu J.C., Xiao B., Naisbitt S., Yuan J.P., Petralia R.S., Brakeman P.,
 RA Doan A., Aakalu V.K., Lananan A.A., Sheng M., Worley P.F.;
 RT "Coupling of mGluR/Homer and PSD-95 complexes by the Shank family of
 RT postsynaptic density proteins.";
 RL Neuron 23:583-592(1999).
 RN [7]
 RP INTERACTION WITH SPTAN1.
 RX MEDLINE=21523912; PubMed=11509555;
 RA Bockers T.M., Maneza M.G., Kreutz M.R., Bockmann J., Weise C.,
 RA Buck F., Richter D., Gundelfinger E.D., Kreienkamp H.-J.;
 RT "Synaptic scaffolding proteins in rat brain. Ankyrin repeats of the
 RT multidomain Shank protein family interact with the cytoskeletal
 RT protein alpha-fodrin.";
 RL J. Biol. Chem. 276:40104-40112(2001).
 RN [8]
 RP FUNCTION.
 RX MEDLINE=21389514; PubMed=11498055;
 RA Sala C., Piech V., Wilson N.R., Passafium M., Liu G., Sheng M.;
 RT "Regulation of dendritic spine morphology and synaptic function by
 RT Shank and Homer.";
 RL Neuron 31:115-130(2001).
 RN [9]
 RP REVIEW.
 RX MEDLINE=20267867; PubMed=10806096;
 RA Sheng M., Kim E.;
 RT "The Shank family of scaffold proteins.";
 RL J. Cell Sci. 113:1851-1856(2000).
 CC -!- FUNCTION: Seems to be an adapter protein in the postsynaptic
 CC density (PSD) of excitatory synapses that interconnects receptors
 CC of the postsynaptic membrane including NMDA-type and metabotropic
 CC glutamate receptors, and the actin-based cytoskeleton. May play a
 CC role in the structural and functional organization of the
 CC dendritic spine and synaptic junction. Overexpression promotes
 CC maturation of dendritic spines and the enlargement of spine heads
 CC via its ability to recruit Homer to postsynaptic sites, and
 CC enhances presynaptic function.
 CC -!- SUBUNIT: May homomultimerize via its SAM domain. Interacts with
 CC SPTAN1, Homer-1 and DLGAP1/GKAP. Is part of a complex with
 CC DLG4/PSD-95 and DLGAP1/GKAP. Interacts with SSTR2 C-terminus via
 CC the PDZ domain (by similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic; postsynaptic density of
 CC neuronal cells. Colocalizes with alpha-latrotoxin receptor 1.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing. Named isoforms=5;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=Q9WV48-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9WV48-2; Sequence=VSP_006072, VSP_006073;
 CC Name=3;
 CC IsoId=Q9WV48-3; Sequence=VSP_006074;
 CC Name=4; Synonyms=A;
 CC IsoId=Q9WV48-4; Sequence=VSP_006075;
 CC Name=5;
 CC IsoId=Q9WV48-5; Sequence=VSP_006076, VSP_006077;
 CC -!- TISSUE SPECIFICITY: Expressed only in brain (neuropil of cortex,
 CC CA1 region hippocampus and molecular layer of cerebellum).
 CC -!- DEVELOPMENTAL STAGE: Expression increases from low levels at birth
 CC to high levels at 3-4 weeks before dropping slightly in adulthood.
 CC Expressed in the cortex and the molecular layer of the cerebellum
 CC at postnatal day 7. Isoform 2 expression does not change during
 CC development of both cortex and cerebellum. Isoform 4 expression
 CC decreases significantly during development of cortex but not
 CC cerebellum.
 CC -!- SIMILARITY: BELONGS TO THE SHANK FAMILY.
 CC -!- SIMILARITY: Contains 7 ANK repeats.
 CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
 CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
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 CC -----
 CC EMBL; AF102855; AAD04569.2; -;
 CC EMBL; AF131951; AAD29417.1; ALT_INIT.
 CC EMBL; AF159046; AAD42975.1; -;
 CC EMBL; AF141904; AAF02498.1; ALT_INIT.
 CC HSSP; P00519; IABL.
 CC InterPro; IPR002110; ANK.
 CC InterPro; IPR001478; PDZ.
 CC InterPro; IPR001660; SAM.
 CC InterPro; IPR001452; SH3.
 CC Pfam; PF00023; ank; 7.

DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00536; SAM; 1.
DR Pfam; PF00018; SH3; 1.
DR ProDom; PRO00066; SH3; 1.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00454; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00088; ANK_REPEAT; 3.
DR PROSITE; PS00297; ANK_REPEAT; 1.
DR PROSITE; PS0106; PDZ; 1.
DR PROSITE; PS0002; SH3; 1.
DR PROSITE; PS0105; SAM_DOMAIN; 1.
KW ANK repeat; SH3 domain; Repeat; Alternative splicing.
FT REPEAT 195 210
FT REPEAT 212 245
FT REPEAT 246 278
FT REPEAT 279 312
FT REPEAT 313 345
FT REPEAT 346 378
FT REPEAT 379 395
FT DOMAIN 554 613
FT DOMAIN 663 757
FT DOMAIN 2104 2167
FT DOMAIN 929 932
FT DOMAIN 1010 1015
FT DOMAIN 1022 1027
FT DOMAIN 1194 1199
FT DOMAIN 1850 1860
FT VARSPLIC 1 613
FT VARSPLIC 615 654
FT VARSPLIC 646 654
FT VARSPLIC 797 804
FT VARSPLIC 1930 1943
FT VARSPLIC 1944 2167
FT CONFLICT 1141 1141
FT CONFLICT 1174 1174
FT CONFLICT 1246 1246
FT CONFLICT 1323 1323
FT CONFLICT 1331 1331
FT CONFLICT 1726 1726
SQ SEQUENCE 2167 AA; 226333 MW; 3F478B5A7B18BA86 CRC64;
Query Match 6.6%; Score 79.5; DB 1; Length 2167;
Best Local Similarity 24.8%; Pred. No. 59;
Matches 40; Conservative 24; Mismatches 50; Indels 47; Gaps 8;
QY 1 MDES-----AKTLPPLCLFCSE---KCEDMKVGVDPITPK-----EEGAVLSS 43
DB 762 MDEAVHKASQQAQKRLPPATSLRSKMTSELEEN-----VSPWKKIYEYQQAAPVS 815
QY 44 SFTMSLYQLAALQADLMNLMELQSYGSAFPAAKU-----LTPAAPRPHN 91
DB 816 MEKKTVVQMALNKLDI-LAAQQTISSESPGGLASLGKHPKGFPPATESFDPHH 874
QY 92 SSRGHRNRAP--PGP-----EETEQQVDLSAPPALR 121
DB 875 RQSPVDRPSFLPPGPGMLRQKSGAEDDRPYLAPPAMK 915
RESULT 11
T160 HUMAN
ID T160 HUMAN STANDARD; PRT; 513 AA.
AC Q92993; Q95624; Q13430; Q9BNK7;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 60 kDa Tat interactive protein (Tip60) (HIV-1 Tat interactive
DE protein) (CPLA2) interacting protein).
GN HTATIP OR TIP60.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lymphoblast;
RX MEDLINE=96182937; PubMed=8607265;
RA Kanine J., Elangovan B., Subramanian T., Coleman D.,
RA Chinnadurai G.;
RT "Identification of a cellular protein that specifically interacts
RT with the essential cysteine region of the HIV-1 tat transactivator.";
RL Virology 216:357-366(1996).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM 2), INTERACTION WITH PLA2G4A, AND
RN SUBCELLULAR LOCATION.
RC TISSUE=Fibroblast, and Placenta;
RX MEDLINE=21309279; PubMed=11416127;
RA Sheridan A.M., Force T., Yoon H.J., O'Leary E., Choukroun G.,
RA Taberi M.R., Bonventre J.V.;
RT "PIP, a novel splice variant of Tip60, interacts with group IV
RT cytosolic phospholipase A(2), induces apoptosis, and potentiates
RT prostaglandin production.";
RL Mol. Cell. Biol. 21:4470-4481(2001).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Cervix;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RN INTERACTION WITH EDNR.
RX PubMed=11262386;
RA Lee H.-J., Chun M., Kandror K.V.;
RT "Tip60 and HDAC7 interact with the endothelin receptor and may be
RT involved in downstream signaling.";
RL J. Biol. Chem. 276:16597-16600(2001).
RN [5]
RN INTERACTION WITH HDAC7.
RX PubMed=12551922;
RA Xiao H., Chung J., Kao H.-Y., Yang Y.-C.;
RT "Tip60 is a co-repressor for STAT3.";
RL J. Biol. Chem. 278:11197-11204(2003).
CC -!- FUNCTION: Binds to the Tat protein of the human immunodeficiency
CC virus (HIV). Specific binding of Tip60 to Tat might be an
CC important feature for efficient Tat transactivation of HIV gene
CC expression.
CC -!- SUBUNIT: Interacts with HIV1 Tat, PLA2G4A/CPLA2, EDNR and HDAC7.
CC -!- SUBCELLULAR LOCATION: Nuclear.

RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Grant C.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-J., McClelland B., Palmieri A.,
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RA "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmle K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lapas C., Markelz B.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RA "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
CC -!- FUNCTION: ASSEMBLES AROUND THE ROD TO FORM THE L-RING AND PROBABLY
CC PROTECTS THE MOTOR/BASAL BODY FROM SHEARING FORCES DURING
CC ROTATION.
CC -!- SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE
CC FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L,P,S, AND M)
CC MOUNTED ON A CENTRAL ROD (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the flgI family.
CC
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CC
CC EMBL; U39941; AAB68970.1; -;
CC DR EMBL; U5165; AAB71792.1; -;
CC DR EMBL; AE009024; AAL41567.1; -;
CC DR EMBL; AE007990; AAK86362.1; -;
CC DR PIR; A97426; A97426.
CC DR HAMAP; MF_00416; -; 1.
CC DR InterPro; IPR001782; Flag_FlgI.
CC DR Pfam; PF01119; FlgI; 1.
CC DR PRINTS; PRO1010; FLGPRINGFLGI.
CC KW Flagella; Periplasmic; Signal; Complete proteome.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 373 FLAGELLAR P-RING PROTEIN.
SQ SEQUENCE 373 AA; 38967 MW; 2BCBC695971CF8A5 CRC64;
Query Match 6.5%; Score 78; DB 1; Length 373;
Best Local Similarity 24.7%; Pred. No. 8;
Matches 56; Conservative 31; Mismatches 84; Indels 56; Gaps 11;
QY 18 EKGEEMK-VGYDPTTPQKEGAVLLSSFTAMSLYQLAALQADLNLRLMELQSVRGSA TP 76
DB 38 QGRNQLIGYGLVGLQGTGSLSSPTEOS-----MRAMLQNLGITGQGGOSNAK 91
QY 77 AAALKLTTPAAPRHNSRGRHNRRAFPQPEETEQVDLSA-----PPALR--NIQDCL--- 128
DB 92 IAAVNVNANLP-PF-----ASPG---SRVDVTYSSLDGATSLAGGNLWTSLSGA 137
QY 129 --QLIADSDTPTIRKGTTFVFWLLSFKRGNALYSQVLYTDPIFAMGHVIOQRKKVHVFGD 186

Db 138 DQIYAVAQGALIVNG-----FSAQGDAAITLQGVTTTSARVPNPAIIRRELPSKPKD 189
QY 187 ELSLVTLFR-----CIGNLEEGDEIQLAIPRENAQIS 218
Db 190 SVNVLQLRPDPFSTAVRVADVNFARARYGDPI--AEPRDSQIEA 234
RESULT 14
VGLZ_HSVKEK STANDARD; PRT; 383 AA.
ID_VGLZ_HSVKEK STANDARD; PRT; 383 AA.
AC P32515; 1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Glycoprotein precursor.
GN US4.
OS Equine herpesvirus type 1 (strain Kentucky A) (EHV-1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92263758; PubMed=1316673;
RA Colle C.F. III, Flowers C.C., O'Callaghan D.J.;
RT "Open reading frames encoding a protein kinase, homolog of
RT glycoprotein gX of pseudorabies virus, and a novel glycoprotein map
RT within the unique short segment of equine herpesvirus type 1.";
RL Virology 188:545-557(1992).
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CC
CC EMBL; M87497; AAA46072.1; -;
CC DR PIR; C42538; VGBEKG.
KW Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 383 GLYCOPROTEIN.
FT DOMAIN 23 75 SER/THR-RICH.
FT TRANSMEM 354 371 POTENTIAL.
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 383 AA; 41027 MW; B390611414131C2B CRC64;
Query Match 6.4%; Score 77.5; DB 1; Length 383;
Best Local Similarity 20.9%; Pred. No. 9.2;
Matches 43; Conservative 24; Mismatches 78; Indels 61; Gaps 8;
QY 73 SATPAAAKLTTPAAPRHNSRGRHNR-----RAFPQPEETEQD VD 113
DB 62 SSPPTSTHTSSPTANAKQKAGHHRGAGRGRRGSPQSGSHTPHPDRLTPSPDYDD-D 120
QY 114 LSAPALPRLNIQDCLLIADSDTPTIRKGTTF-----VPMWL----- 151
DB 121 TNHENGNNISIEIVQL--PPDRPIELGVATLTKRNFMEASCTVETNSDLAIFWKIGKPS 178
QY 152 --SPKRGNALYSQVLYTDPIFAMGHVIOQRKKVHVFGDELSLVTLFRICNLNLEEGDEIQL- 208
DB 179 VDAFNRGTTHRLMRNGVPYVALVTLRVFPLNVI--PLTKITCAACPTNLVAGDGVLDN 236
QY 209 -----AIP-----RENAQISRNGD 222
DB 237 SCTTKSTTTPCPCQQRTHIFPSAKGD 262
RESULT 15
YAPI_HUMAN STANDARD; PRT; 454 AA.
ID_YAPI_HUMAN
AC P46937;

Search completed: February 3, 2004, 07:44:16
Job time : 11.7956 secs

DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 65 kDa Yes-associated protein (YAP65).
GN YAP1 OR YAP65.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=95301570; PubMed=7782338;
RA Sudol M., Bork P., Einbond A., Kastury K., Druck T., Negrini M.,
RA Huebner K., Lehman D.;
RT "Characterization of the mammalian YAP (Yes-associated protein) gene
and its role in defining a novel protein module, the WW domain.";
RL J. Biol. Chem. 270:14733-14741(1995).
RN [2]
RP INTERACTION WITH WBP1 AND WBP2.
RX MEDLINE=97347517; PubMed=9202023;
RA Chen H.I., Einbond A., Kwak S.-J., Linn H., Koepf E., Peterson S.,
RA Kelly J.W., Sudol M.;
RT "Characterization of the WW domain of human Yes-associated protein and
its polyproline containing ligands.";
RL J. Biol. Chem. 272:17070-17077(1997).
CC -!- SUBUNIT: Binds to the SH3 domain of the YES kinase. Binds to WBP1
and WBP2.
CC -!- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC -!- SIMILARITY: Contains 1 WW domain.
CC -----
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DR EMBL; X80507; CAA56672.1; -.
DR FIR; A56954; A56954.
DR PDB; 1JMQ; 21-DEC-01.
DR PDB; 1K9Q; 28-DEC-01.
DR PDB; 1K9R; 28-DEC-01.
DR Genew; HGNC:16262; YAP1.
DR MIM; 606608.
DR GO; GO:0005515; F:protein binding activity; TAS.
DR InterPro; IPR005153; MbCh.
DR InterPro; IPR001202; WW_Rsp5_WWP.
DR Pfam; PF00397; WW; 1.
DR SMART; SM00456; WW; 1.
DR PROSITE; PS01159; WW_DOMAIN_1; 1.
DR PROSITE; PS00200; WW_DOMAIN_2; 1.
KW Phosphorylation; 3D-Structure.
FT DOMAIN 171 204 WW.
SQ SEQUENCE 454 AA; 48755 NW; 87CB840D3393EFC0 CRC64;
Query Match 6.4%; Score 77.5; DB 1; Length 454;
Best Local Similarity 20.8%; Pred. No. 12;
Matches 30; Conservative 16; Mismatches 61; Indels 37; Gaps 3;
QY 1 MDESAKTLPPPCLCFCSEKEDMKVGYDPTTPQKEGAVLLSSFTAMSLYQLAALQADL 60
Db 235 ISQSAPVKQPP-----PLAQSPQGGVGGSGNSNQOQMRLOQLEK 277
QY 61 MNLRMELQSYRGSAIPAALKLTPAAPRHNSRGRHNRRAFPPEETEEDVLSAPPAL 120
Db 278 ERLRLKQQLLRQVRPELAL-----RSQLP---TLEQDGGTGNPVSS 317
QY 121 RNIIQDCLQLIADSDTPTIRKGY 144
Db 318 PGMQSGLRTMTTNSDPLNSGTY 341

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:43:37 ; Search time 30.9333 Seconds
(without alignments)
1935.395 Million cell updates/sec

Title: US-09-911-777-2

Perfect score: 1204

Sequence: 1 MDESARTLPPCLCFCSERK.....ENAIQRNGDDTFFGALKLL 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

- 1: sp_archea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	909	75.5	258	11 Q8BZM8	Q8BZM8 mus musculus
2	674.5	56.0	199	11 Q8BWP2	Q8BWP2 mus musculus
3	673.5	55.9	194	11 Q8BVA3	Q8BVA3 mus musculus
4	541.5	45.0	208	4 Q8IZI6	Q8IZI6 homo sapien
5	522	43.4	174	4 Q8IZI5	Q8IZI5 homo sapien
6	490	40.7	158	4 Q8IZI4	Q8IZI4 homo sapien
7	430.5	35.8	288	13 Q8JHJ4	Q8JHJ4 gallus gall
8	152	12.6	410	11 Q8BXS2	Q8BXS2 mus musculus
9	149	12.4	250	4 Q8NPH7	Q8NPH7 homo sapien
10	127	10.5	330	4 Q8IZK7	Q8IZK7 homo sapien
11	91	7.6	793	4 Q13876	Q13876 homo sapien
12	89	7.4	420	16 Q8RJO6	Q8RJO6 streptomyce
13	88	7.3	402	4 Q8NVB6	Q8NVB6 homo sapien
14	88	7.3	402	4 Q9H7U5	Q9H7U5 homo sapien
15	88	7.3	542	4 Q8N543	Q8N543 homo sapien
16	88	7.3	542	4 Q9H9J9	Q9H9J9 homo sapien

17	88	7.3	542	4 Q9HA87	Q9HA87 homo sapien
18	88	7.3	550	4 Q9HCG0	Q9HCG0 homo sapien
19	85.5	7.1	442	2 Q9F6X7	Q9F6X7 chloroflexu
20	85.5	7.1	1066	16 Q8G5I3	Q8G5I3 bifidobacte
21	85	7.1	767	13 Q9I2I5	Q9I2I5 oncorhynchu
22	84.5	7.0	239	9 Q8SDX2	Q8SDX2 bacterioph
23	84.5	7.0	380	16 P95190	P95190 mycobacteri
24	84.5	7.0	986	4 Q9UPW8	Q9UPW8 homo sapien
25	83.5	6.9	441	2 Q07386	Q07386 lactococcus
26	83	6.9	574	2 Q8VQX9	Q8VQX9 myxococcus
27	83	6.9	1075	3 Q8NJ74	Q8NJ74 ustilago ma
28	82.5	6.9	240	10 Q8LFZ7	Q8LFZ7 arabidopsis
29	82.5	6.9	404	4 Q8NAL3	Q8NAL3 homo sapien
30	82.5	6.9	1119	5 Q9U2G5	Q9U2G5 caenorhabdi
31	82	6.8	513	11 Q8VIH0	Q8VIH0 mus musculu
32	81.5	6.8	967	5 Q8I540	Q8I540 plasmodium
33	81	6.7	397	11 Q8K0U6	Q8K0U6 mus musculu
34	81	6.7	891	5 Q01525	Q01525 caenorhabdi
35	81	6.7	1333	11 Q8CHB8	Q8CHB8 mus musculu
36	80.5	6.7	253	10 Q40898	Q40898 petunia hyb
37	80.5	6.7	678	11 Q8JZP9	Q8JZP9 mus musculu
38	80.5	6.7	1735	11 Q62768	Q62768 rattus norv
39	80	6.6	567	11 Q8CIA2	Q8CIA2 mus musculu
40	80	6.6	944	5 Q8T4E9	Q8T4E9 drosophila
41	80	6.6	1776	5 Q8MQW8	Q8MQW8 drosophila
42	80	6.6	1776	5 Q9BK48	Q9BK48 drosophila
43	80	6.6	1776	5 Q9W2T7	Q9W2T7 drosophila
44	80	6.6	1790	5 Q9BK49	Q9BK49 drosophila
45	80	6.6	4379	2 Q9RAH4	Q9RAH4 nostoc sp.

ALIGNMENTS

RESULT 1

Q8BZM8 PRELIMINARY; PRT; 258 AA.
ID Q8BZM8;
AC Q8BZM8;
DT 01-MAR-2003 (TREMREL. 23, Created)
DT 01-MAR-2003 (TREMREL. 23, Last sequence update)
DT 01-MAR-2003 (TREMREL. 23, Last annotation update)
DE Tumor necrosis factor (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK034121; BAC28593.1;
FT NON_TER
SQ SEQUENCE 258 AA; 28604 MW; E6431FE93E782810 CRC64;

Query Match 75.5%; Score 909; DB 11; Length 258;

Best Local Similarity 75.9%; Pred. No. 7.1e-83;

Matches: 192; Conservative 0; Mismatches 1; Indels 60; Gaps 4;

QY	40	LLSSFTAMSLYQLAALQADLNLMELQSYRGSAAPAA-----KLLTPAAPRP 90
DB	6	LLSSFTAMSLYQLAALQADLNLMELQSYRGSAAPAAPELTAGVKLLTPAAPRP 65
QY	91	NSSRGHRNRAPPGPEETEQQVDLSAPPA-----LRNIQDCIQLIAD 133
DB	66	NSSRGHRNRAPPGPEETEQQVDLSAPPAPELTAGVKLRHSQHDGNGNLRNIQDCIQLIAD 125
QY	134	SDTPTIRKGTTFVFPWLLSFRKGNAL-----YSQVLYTDPFAMGHVI 176

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4 Q
5 Q
Db 126 SDTPTIRKGTGTYFVFWLLSFKRGNALBKENKIVVQRTGYFFYISQVLYTDPFAMGHVI 185
Qy 177 QKQKVHVFGDELSLVTFRQON-----LEEGDEIQALAIAPRENAQISR 219
Db 186 QKQKVHVFGDELSLVTFRQONPKPTLPNNSCYSAGIARLEEGDEIQALAIAPRENAQISR 245
Qy 220 NGDDTFFGALKLL 232
Db 246 NGDDTFFGALKLL 258

RESULT 2
Q8BWP2 PRELIMINARY; PRT; 199 AA.
ID Q8BWP2;
AC Q8BWP2;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Tumor necrosis factor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK050384; BAC34225.1; -.
SQ SEQUENCE 199 AA; 21654 MW; 39392021D4EFD320 CRC64;

Query Match 56.0%; Score 674.5; DB 11; Length 199;
Best Local Similarity 75.3%; Pred. No. 1.7e-59;
Matches 140; Conservative 1; Mismatches 2; Indels 43; Gaps 3;

Qy 1 MDESATLPPPCLCFCSEKGEDMKVGYDPTTPQKEGA-----VLLSS 43
Db 1 MDESATLPPPCLCFCSEKGEDMKVGYDPTTPQKEGAWFGICRDGRLLAATLLALLSS 60
Qy 44 SFTMSLYQLAALQADLMLNLMELQSYRGSATPAA-----KLTPAAPRPHNSSR 94
Db 61 SFTMSLYQLAALQADLMLNLMELQSYRGSATPAAAGAPELTAGVKLLTPAAPRPHNSSR 120
Qy 95 GHRNRAPPGPEETEODVDLSAPPA-----LRNIQDCLQLIADSDTP 137
Db 121 GHRNRAPPGPEETEODVDLSAPPAWFGICRDGRLLAATLLALLSS 180
Qy 138 TIRKGT 143
Db 181 TIRKGS 186

RESULT 3
Q8BVA3 PRELIMINARY; PRT; 194 AA.
ID Q8BVA3;
AC Q8BVA3;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Tumor necrosis factor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,

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RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK079180; BAC37571.1; -.
SQ SEQUENCE 194 AA; 20961 MW; 85FCF3495B138377 CRC64;

Query Match 55.9%; Score 673.5; DB 11; Length 194;
Best Local Similarity 75.7%; Pred. No. 2e-59;
Matches 140; Conservative 0; Mismatches 2; Indels 43; Gaps 3;

Qy 1 MDESATLPPPCLCFCSEKGEDMKVGYDPTTPQKEGA-----VLLSS 43
Db 1 MDESATLPPPCLCFCSEKGEDMKVGYDPTTPQKEGAWFGICRDGRLLAATLLALLSS 60
Qy 44 SFTMSLYQLAALQADLMLNLMELQSYRGSATPAA-----KLTPAAPRPHNSSR 94
Db 61 SFTMSLYQLAALQADLMLNLMELQSYRGSATPAAAGAPELTAGVKLLTPAAPRPHNSSR 120
Qy 95 GHRNRAPPGPEETEODVDLSAPPA-----LRNIQDCLQLIADSDTP 137
Db 121 GHRNRAPPGPEETEODVDLSAPPAWFGICRDGRLLAATLLALLSS 180
Qy 138 TIRKGT 142
Db 181 TIRKGS 185

RESULT 4
Q8IZI6 PRELIMINARY; PRT; 208 AA.
ID Q8IZI6;
AC Q8IZI6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE B-lymphocyte stimulator (Fragment).
GN TNFSF13B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gao H., He F., Li R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY129226; AA08422.1; -.
FT NON TER
SQ SEQUENCE 208 AA; 22767 MW; EEA31D227033AA53 CRC64;

Query Match 45.0%; Score 541.5; DB 4; Length 208;
Best Local Similarity 53.2%; Pred. No. 3.9e-46;
Matches 118; Conservative 14; Mismatches 25; Indels 65; Gaps 4;

Qy 62 NLRMELQSYRGSATPAA-----KLTPAAPRPHNSSRGRNRAPPG 104
Db 1 SLRAELQGHHAELPAGAGAPKAGLEBAPVATGKIFEPAPGEGNSSQSNRKAQVG 60
Qy 105 PEETEODVDLSAPPALRNIIQDCLQLIADSDTPPIRGTGTYFVFWLLSFKRGNAL----- 159
Db 61 PEET-----VTQDCLQLIADSETPTIQGSYTFVFWLLSFKRGSALAEKEN 106
Qy 160 -----YSQVLYTDPFAMGHVIOKKVHVFGDELSLVTFRQON----- 199
Db 107 KILVETGYFFYQVLYTKTYAMGHVIOKKVHVFGDELSLVTFRQONMETLPPN 166
Qy 200 -----LEEGDEIQALAIAPRENAQISRNGDDTFFGALKLL 232
Db 167 SCYSAGIAKLEEGDELQITIPRENAQISLDGDTFFGALKLL 208

RESULT 5
Q8IZI5 PRELIMINARY; PRT; 174 AA.
ID Q8IZI5

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[illegible]

RL Nature 420:563-573(2002).
DR EMBL: AK044387; BAC31897.1; -- 590A4B74C33PB8D4 CRC64;
SQ SEQUENCE 410 AA; 45881 MW; 590A4B74C33PB8D4 CRC64;

Query Match 12.6%; Score 152; DB 11; Length 410;
Best Local Similarity 27.0%; Pred. No. 1.1e-06;
Matches 62; Conservative 22; Mismatches 70; Indels 76; Gaps 8;

QY 52 QLAALQADLMNLEMLQSYRGSATPAAKLLTPAAPRHNS-----SRGHR 97
DB 207 QRLCQTELOSLRREVSRLQSGGSPQXQ-----GERPWQSLWEQSPVLEAWKDGAKSR 261
QY 98 NRRAPPGPEETQDQVLSAPPALRNIIQDCLQIADSDTPTIRKGTGTYFVPWLLSFKRG 157
DB 262 RRAVLTQKHKHSHVLPV--NITSK-----ADSDV-----TEVMQPVLRGR 306
QY 158 A-----LYSOVLYTDPIFAMGHVQIRKKVHVFGEDELSTLTPFCIQ-- 198
DB 307 GLEAQGDIVRVWDTGYLLYSQVLFHDVFTFTMGQVVSRE-----GQGRRETLFCIRSM 360
QY 199 -----NLEEGDEIQALIPRENAQISRGNGDDTFPGALKL 231
DB 361 PSDPRAYNCSYAGVFLHQGDILITVXIPRANAKLSLSPHGTFLGFKL 410

RESULT 9

Q8NFH7 PRELIMINARY; PRT; 250 AA.
ID Q8NFH7
AC Q8NFH7
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Proliferation-inducing ligand APRIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyama T., Tsukamoto H., Masumoto K., Himeji D., Hayaashi K.,
RA Harada M., Horiuchi T.;
RL "Genomic structure of APRIL, a proliferation-inducing ligand.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF513501; AAM47279.1; --
DR InterPro; IPR006052; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS0049; TNF 2; 1.
SQ SEQUENCE 250 AA; 27453 MW; AE1E4FDEFD578898 CRC64;

Query Match 12.4%; Score 149; DB 4; Length 250;
Best Local Similarity 25.9%; Pred. No. 1.2e-06;
Matches 58; Conservative 27; Mismatches 73; Indels 66; Gaps 7;

QY 53 LAALQADLMNLEMLQSYRGSATPAAKLLTPAAPRHNS-----RGHRNRAPP 103
DB 48 LTOQTELOSLRREVSRLQSGGSPQXQ-----GERPWQSLWEQSPVLEAWKDGAKSR 107
QY 104 GPEETEQQDQVLSAPPALRNIIQDCLQIADSDTPTIRKGTGTYFVPWLLSFKRGNA----- 158
DB 108 TQKQKQSHVLPV--INATSK-----DSVD-----TEVMQPALRRGRGLQAG 152
QY 159 -----LYSOVLYTDPIFAMGHVQIRKKVHVFGEDELSTLTPFCIQ----- 198
DB 153 YGVRIQDAGVYLLYSQVLFHDVFTFTMGQVVSRE-----GQGRRETLFCIRSM 206
QY 199 -----NLEEGDEIQALIPRENAQISRGNGDDTFPGALKL 231
DB 207 AYNSCYSGVFLHQGDILSVIIPRANAKLSLSPHGTFLGFKL 250

RESULT 10

QY 29 FITQKEEGAVLLSSFTMSLYQL-----AALQADLMNLEMLQSYRGSATPAAKLL 82

Q81ZK7 PRELIMINARY; PRT; 330 AA.
ID Q81ZK7
AC Q81ZK7
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE TWE-PRIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22299924; PubMed=12411489;
RA Prader-Balade B., Medena J.P., Lopez-Fraga M., Lozano J.C.,
RA Kofschoten G.M., Picard A., Martinez-A C., Garcia-Sanz J.A.,
RA Hahne M.;
RT "An endogenous hybrid mRNA encodes TWE-PRIL, a functional cell surface
RT TWEAK-APRIL fusion protein.";
RL EMBO J. 21:5711-5720(2002).
DR EMBL: AY081051; AAL90443.1; --
SQ SEQUENCE 330 AA; 36588 MW; FC6F3BCA29C029AE CRC64;

Query Match 10.5%; Score 127; DB 4; Length 330;
Best Local Similarity 27.1%; Pred. No. 0.00027;
Matches 48; Conservative 21; Mismatches 50; Indels 58; Gaps 7;

QY 91 NSSRGHNRRAFPQPEETEQQDQVLSAPPALRNIIQDCLQIADSDTPTIRKGTGTYFVPWL 150
DB 176 NGERS-RKRAVLTQKQKQSHVLPV--INATSK-----DSVD-----TEVMQ 219
QY 151 LSFKRGNA-----LYSOVLYTDPIFAMGHVQIRKKVHVFGEDELSTL 193
DB 220 PALRRGRGLQAGVGVRIQDAGVYLLYSQVLFQDVFTMGQVVSRE-----GQGRQETL 273
QY 194 FRCIQ-----NLEEGDEIQALIPRENAQISRGNGDDTFPGALKL 231
DB 274 FRCIRSMPSHDPDRAYNCSYAGVFLHQGDILSVIIPRANAKLSLSPHGTFLGFKL 330

RESULT 11

Q13876 PRELIMINARY; PRT; 793 AA.
ID Q13876
AC Q13876
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Bone-derived growth factor (Fragment).
GN BPGF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gao C., Zhou H.E., Chen B.-Q., Chung L.W.K.;
RT "Molecular cloning and expression of A novel bone-derived growth
RT factor from a human osteosarcoma cell line.";
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: L42379; AAA89173.1; --
DR HSSP; P00274; 1F6M.
DR Genew; HGNC:9756; OSCN6.
DR InterPro; IPR006662; Thioired.
DR InterPro; IPR006663; Thioiredox_dom2.
DR Pfam; PF00085; thioired; 1.
FT NON TER 1
SQ SEQUENCE 793 AA; 86395 MW; 7418928B218A7B62 CRC64;

Query Match 7.6%; Score 91; DB 4; Length 793;
Best Local Similarity 22.7%; Pred. No. 3.5;
Matches 58; Conservative 25; Mismatches 81; Indels 92; Gaps 13;

Db 535 PTPSQ-----ATSWTSLSQLGOLPEGCACAAAPELAMGALELESRNSTLDPKPEMM 587
QY 83 -TPAAPRPHNSRG-----HRNRAPPGPE-----ETEODVLS----- 115
Db 588 KSPTTTHVPAEGEASPPKHLPGCLRAAPQEPPEHADVQORNEQDFLQWHLRSET 647
QY 116 -----APPALRNIIQDCILQIADSDTPTIRKGTTFVP--WLLGPK-----RGNALY 160
Db 648 QGLHCWLSPLGRLTASGALW-----RSGAWAASPSSWSTSLRPAGGSPWTRGQW 697
QY 161 SOV-----LYTDPFAMGHVIOKKVHVP-GBELSVTLFRCIQNLBEGD 204
Db 698 LQVLOGGFSYLDISLGVLPSCWACW-----VHLLPGQDKALNRMLATLOPEPGE 751
QY 205 EQLAIPRENAOISRN 220
Db 752 E-----AGEGAISRH 762

RESULT 12
Q9RJQ6 PRELIMINARY; PRT; 420 AA.
AC Q9RJQ6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Putative cytochrome P450 157B1.
GN CYP157B1 OR SCO0584 OR SCF55.08C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kisser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939106; CAB61278.1; --
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 420 AA; 45888 MW; F7FE250A4895A640 CRC64;

Query Match 7.4%; Score 89; DB 16; Length 420;
Best Local Similarity 29.5%; Pred. No. 2.4;
Matches 38; Conservative 16; Mismatches 45; Indels 30; Gaps 7;
QY 62 NRMELQYRGSAATPAAKLITPAAPRPHNSRGHNRRAFPGPDETDVLSAPPALR 121
Db 189 DLRLSLDAEGD-DFVAA--YTRVGERIHQLVRKKRER---PGPDVTSRMLTHPAGLTDE 242
QY 122 NIIOCLQIADSDTPTIRKGTTFVPWLLSFKRNALYSQVLYTDPFAMGHVIOKKV 181
Db 243 EIVQDLISVIAAQOPTAN-----WI-----GNTL--RLLLTDERPAL----- 278
QY 182 HVFGDELSL 190
Db 279 NVSGGRLSV 287

RESULT 13
Q9NVB6 PRELIMINARY; PRT; 402 AA.
AC Q9NVB6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ10826.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsumura H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahara K., Masuho Y., Sasaki N.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK001688; BAA91838.1; --
KW Hypothetical protein.
SQ SEQUENCE 402 AA; 46851 MW; BC09C12945BE8146 CRC64;

Query Match 7.3%; Score 88; DB 4; Length 402;
Best Local Similarity 26.1%; Pred. No. 2.8;
Matches 30; Conservative 17; Mismatches 42; Indels 26; Gaps 4;
QY 18 EKGDMKGVDPITPQ-----KEGAVLLSSFTAMSLYQLAALQADLMNLRMELQ 68
Db 190 EKAEESKL-----PEILKECMKLFPSALFLLLSNFTGLKHLFLAPSEDEMNDKKEAE 243
QY 69 SYRGSAATPAAKLITPAAPRPHNSRG-----HRNRAPFGPDETDVLSAP 117
Db 244 T-----TDITEGTHSPPEPENNQMAISNNQSQSQSQSQSQSQSQSQSQSQSQSQSQ 293

RESULT 14
Q9H7U5 PRELIMINARY; PRT; 402 AA.
AC Q9H7U5;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ14252.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovarian carcinoma;
RA Isogai T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

RA	Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA	Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA	Yamanoto J., Wakamatsu A., Nakamura Y., Nagahari K., Maeuho Y.,
RT	Ninomiya K., Iwayanagi T.;
RT	"NEDO human cDNA sequencing project.";
RL	Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AK024314; BAB14890.1; -;
DQ	Hypothetical protein.
SQ	SEQUENCE 402 AA; 46789 MW; OD62A85B40B9AC33 CRC64;
Query Match 7.3%; Score 88; DB 4; Length 402;	
Best Local Similarity 26.1%; Pred. No. 2.8;	
Matches 30; Conservative 17; Mismatches 42; Indels 26; Gaps 4;	
QY	18 EKGEDMKVGYDPTTPQ-----KEEGAVLLSSSTFMSLYQLAALQADLMNLRMELQ 68 : : : : : : : : : : : : : : : : : :
Db	190 EKAESKL-----PEILKCEMCLFRSEALFLLSNFTGLKLHFLAPSEEDMDKKAE 243 : : : : : : : : : : : : : : : : : :
QY	69 SYGGSATPAAAKLLTPAAPHPNSSRG-----HRNRRAFGPGPETQDDVLSP 117 : : : : : : : : : : : : : : : : : :
Db	244 T-----TDITEGTSHSGPPENQMAISNNQSQQSNEQTDPDENETKKESSVP 293 : : : : : : : : : : : : : : : : : :
RESULT 15	
QBN543	PRELIMINARY; PRT; 542 AA.
ID	QBN543
AC	QBN543;
DT	01-OCT-2002 (TEmBLrel. 22, Created)
DT	01-OCT-2002 (TEmBLrel. 22, Last sequence update)
DE	01-MAR-2003 (TEmBLrel. 23, Last annotation update)
DE	Hypothetical protein FLJ10826.
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RC	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RL	Strausberg R.;
RL	Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC032919; AAH32919.1; -;
DR	Interpro; IPR006620; Pro_4_hyd_alpha.
DR	SMART; SM00702; P4HC; 1.
KW	Hypothetical protein.
SQ	SEQUENCE 542 AA; 8834BB200D5D8D85 CRC64;
Query Match 7.3%; Score 88; DB 4; Length 542;	
Best Local Similarity 26.1%; Pred. No. 4.2;	
Matches 30; Conservative 17; Mismatches 42; Indels 26; Gaps 4;	
QY	18 EKGEDMKVGYDPTTPQ-----KEEGAVLLSSSTFMSLYQLAALQADLMNLRMELQ 68 : : : : : : : : : : : : : : : : : :
Db	330 EKAESKL-----PEILKCEMCLFRSEALFLLSNFTGLKLHFLAPSEEDMDKKAE 383 : : : : : : : : : : : : : : : : : :
QY	69 SYGGSATPAAAKLLTPAAPHPNSSRG-----HRNRRAFGPGPETQDDVLSP 117 : : : : : : : : : : : : : : : : : :
Db	384 T-----TDITEGTSHSGPPENQMAISNNQSQQSNEQTDPDENETKKESSVP 433 : : : : : : : : : : : : : : : : : :

Search completed: February 3, 2004, 07:46:52
Job time : 32.9333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:43:37 ; Search time 38.6667 Seconds
(without alignments)
952.359 Million cell updates/sec

Title: US-09-911-777-2

Perfect score: 1204

Sequence: 1 MDEGAKTLPPCLFCSEK.....ENAIQRNGDDTFFGALKLL 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1103.5	91.7	309	21	AA197039
2	1103.5	91.7	309	23	ABG96469
3	1103.5	91.7	309	23	ABJ00717
4	1103.5	91.7	309	23	ABP47219
5	1103.5	91.7	309	23	ABG33578
6	1103.5	91.7	309	23	AAU79147
7	1103.5	91.7	309	23	AAU10943
8	1097.5	91.2	309	21	AA108262
9	999	83.0	290	20	AA104393

10	999	83.0	290	20	AAW93587	Mouse TNFL1-alpha
11	999	83.0	290	22	AAE07880	Mouse BAPF protein
12	999	83.0	290	23	ABG96470	Mouse Neutrokine-a
13	999	83.0	290	23	ABJ00718	Murine B lymphocyt
14	999	83.0	290	23	ABP47220	Human BlyS binding
15	999	83.0	290	23	ABG33579	Murine B lymphocyt
16	999	83.0	290	23	AAU79148	Mouse Neutrokine-a
17	992.5	82.4	289	23	ABG96468	Mouse Neutrokine-a
18	992.5	82.4	289	23	AAE26219	Mouse neutrokine-a
19	780.5	64.8	239	23	ABJ00719	Rat B lymphocyte s
20	780.5	64.8	239	23	ABP47221	Human BlyS binding
21	780.5	64.8	239	23	ABG33580	Rat B lymphocyte s
22	723.5	60.1	207	23	ABJ00721	Rat B lymphocyte s
23	723.5	60.1	207	23	ABP47223	Human BlyS binding
24	723.5	60.1	207	23	ABG33582	Rat B lymphocyte s
25	681	56.6	220	23	ABJ00720	Rat B lymphocyte s
26	681	56.6	220	23	ABP47222	Human BlyS binding
27	681	56.6	220	23	ABG33581	Rat B lymphocyte s
28	625	51.9	188	23	ABJ00722	Rat B lymphocyte s
29	625	51.9	188	23	ABP47224	Human BlyS binding
30	625	51.9	188	23	ABG33583	Rat B lymphocyte s
31	622.5	51.7	285	19	AAW73043	Tumour necrosis fa
32	622.5	51.7	285	19	AAW62461	Human T cell surfa
33	622.5	51.7	285	19	AAW58391	Homo sapiens neutr
34	622.5	51.7	285	20	AAW22221	Human TNFL1 protei
35	622.5	51.7	285	20	AAW04392	Human Kay-1 ligand
36	622.5	51.7	285	20	AAW93586	Human TNFL1-alpha
37	622.5	51.7	285	21	AAW28553	Human TNFL1
38	622.5	51.7	285	21	AAW08659	Amino acid sequenc
39	622.5	51.7	285	21	AAW08191	Amino acid sequenc
40	622.5	51.7	285	21	AAW08261	Amino acid sequenc
41	622.5	51.7	285	22	AAE09242	Human TALL-1 prote
42	622.5	51.7	285	22	AAE07156	Human tumour necro
43	622.5	51.7	285	22	AAE07879	Human BAPF protein
44	622.5	51.7	285	22	AAU12183	Human PRO738 polyp
45	622.5	51.7	285	22	AAW71915	Human TAC1-ligand

ALIGNMENTS

RESULT 1

AA197039

ID AA197039 standard; Protein; 309 AA.

XX AA197039;

DT 31-OCT-2000 (first entry)

DE Membrane bound murine TNF ligand T7.

KW TNF; membrane bound; tumour necrosis factor ligand; D7; trimer;
KW NF-kappa-B; modulator; CD40 inducer; gene therapy; vaccine; adjuvant;
KW cytotostatic; immunosuppressive; antibacterial; antiviral;
KW immunomodulator.

OS Mus sp.

XX

Key Location/Qualifiers

Domain 49..70

FT Modified-site 266

FT /label= Transmembrane_domain

FT /note= "Potential N-linked glycosylation site"

XX WO200039295-A1.

PN

XX Mouse Neutrokine-a

PD 06-JUL-2000.

XX Human BlyS binding

PF 05-OCT-1999; 99WO-EP07303.

XX Mouse Neutrokine-a

PR 23-DEC-1998; 98GB-0028628.

XX Amino acid sequenc

PA (GLAXO) GLAXO GROUP LTD.

XX Farrow SN, Kaptein A, Kitson JDA, Winder AJ;
 XX WPI; 2000-452393/39.
 DR N-PSDB; AAA51863.
 XX
 XX New member of the tumor necrosis factor ligand family, known as the D7
 PT ligand, useful in treating cancer, autoimmune disease or diseases
 PT associated with the activation of NF-kappaB
 XX
 XX Disclosure; Fig 6; 48pp; English.
 XX
 XX This is the membrane bound murine tumour necrosis factor (TNF)
 CC ligand, D7, D7 or D7 trimers are useful in immunotherapy or treatment of
 CC cancer. D7 is useful against viral diseases or infections, or as a
 CC vaccine adjuvant. It may also be used as an immunogen to produce
 CC antibodies or for screening methods, e.g. for identifying modulators of
 CC D7-receptor interaction. Modulators are useful for immunotherapy,
 CC particularly, in treating inflammation, autoimmune disease, other
 CC diseases associated with activation of transcription factor NF-kappa-B
 CC (e.g. rheumatoid arthritis, neuronal inflammation, asthma), cancers,
 CC infections (e.g. septic shock), or atherosclerosis. The D7 gene is useful
 CC in gene therapy, and may be employed for producing the protein by
 CC recombinant techniques. D7 antibodies are useful for locating the protein
 CC in a tissue, or for purifying the protein.
 XX
 XX SQ Sequence 309 AA;
 Query Match 91.7%; Score 1103.5; DB 21; Length 309;
 Best Local Similarity 74.4%; Pred. No. 3.2e-116;
 Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;
 QY 1 MDESATLPPPCLCFCSEKGEKMDKGYDPTPQKEGA-----VLSS 43
 DB 1 MDESATLPPPCLCFCSEKGEKMDKGYDPTPQKEGA-----VLSS 60
 QY 44 SFTMSLVQLAALQADLNLRLMELQSYRGSATPAAA-----KLTPAAPRPHNSR 94
 DB 61 SFTMSLVQLAALQADLNLRLMELQSYRGSATPAAAGAPELTAGVKLLTPAAPRPHNSR 120
 QY 95 GHRNRRAPPGPTEQDDVLSAPPA-----LRNIIQDCLQLIADSDTP 137
 DB 121 GHRNRRAPPGPTEQDDVLSAPPAAPCLPGCRHSQDDNGMNLNIIQDCLQLIADSDTP 180
 QY 138 TIRKGTTFVFWLLSKFGNAL-----YSQVLYTDFIFANGHVIQKK 180
 DB 181 TIRKGTTFVFWLLSKFGNAL-----YSQVLYTDFIFANGHVIQKK 240
 QY 181 VHVFGDELSTLVTLFRQION-----LEEGDEIQLAIPRENAQISRNGDD 223
 DB 241 VHVFGDELSTLVTLFRQIONWPKTLPNNSCYSAGIARLEBGEIQLAIPRENAQISRNGDD 300
 QY 224 TFFGALKL 232
 DB 301 TFFGALKL 309
 RESULT 2
 ABG96469
 ID ABG96469 standard; Protein; 309 AA.
 XX
 XX AC ABG96469;
 XX
 XX 11-DEC-2002 (first entry)
 XX
 XX Mouse Neutrokin-alpha-like protein fragment #2.
 KW Neutrokin-alpha; cytokine; autoimmune disease; cancer;
 KW systemic lupus erythematosus; rheumatoid arthritis; Sjogren's syndrome;
 KW B cell cancer; chronic lymphocytic leukaemia; multiple myeloma;
 KW Hodgkin's lymphoma; non-Hodgkin's lymphoma; immunodeficiency;
 KW hypergammaglobulinaemia; hypogammaglobulinaemia; rheumatic heart disease;
 KW diabetes mellitus; autoimmune thyroiditis; Goodpasture's syndrome;

KW Graves' disease; myasthenia gravis; autoimmune haemolytic anaemia;
 KW infertility; chronic active hepatitis; primary biliary cirrhosis;
 KW inflammatory skin disease; psoriasis; allergy; atherosclerosis;
 KW autoimmune thrombocytopaenia; antibody; chromosome 13q34.

OS Mus musculus.

PN US2002115112-A1.

XX 22-AUG-2002.

XX 15-AUG-2001; 2001US-0929493.

XX 22-FEB-2000; 2000US-0507968.

PR 02-MAR-1999; 99US-122388P.

PR 12-MAR-1999; 99US-124097P.

PR 26-MAR-1999; 99US-126599P.

PR 02-APR-1999; 99US-127598P.

PR 16-APR-1999; 99US-130412P.

PR 23-APR-1999; 99US-130696P.

PR 27-APR-1999; 99US-131278P.

PR 29-APR-1999; 99US-131673P.

PR 28-MAY-1999; 99US-136784P.

PR 06-JUL-1999; 99US-142659P.

PR 03-DEC-1999; 99US-168624P.

PR 16-DEC-1999; 99US-171108P.

PR 23-DEC-1999; 99US-171626P.

PR 14-JAN-2000; 2000US-176015P.

PR 15-AUG-2000; 2000US-225628P.

PR 23-AUG-2000; 2000US-227008P.

PR 22-SEP-2000; 2000US-234338P.

PR 17-OCT-2000; 2000US-240806P.

PR 30-NOV-2000; 2000US-250020P.

PR 07-JUN-2001; 2001US-296122P.

PR 13-JUL-2001; 2001US-304809P.

PR 22-FEB-2000; 2000US-0507968.

PR 02-JUN-2000; 2000US-0586288.

PR 08-JUN-2000; 2000US-0588947.

PR 08-JUN-2000; 2000US-0589285.

PR 08-JUN-2000; 2000US-0589286.

PR 08-JUN-2000; 2000US-0589287.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Yu G, Ebner R, Ni J, Rosen CA, Ullrich S;

XX WPI; 2002-740098/80.

XX Novel antibody that binds to neurokinine-alpha protein, useful for
 PT diagnosing and treating diseases or disorders, such as autoimmune
 PT diseases, lupus erythematosus, rheumatoid arthritis, cancer, or an
 PT immunodeficiency -

Disclosure; Page 172; 203pp; English.

XX The invention relates to an isolated antibody (I) or its portion that
 CC specifically binds to a 285 residue neurokinine-alpha protein sequence
 CC or a 250 residue APRIL (proliferation inducing ligand) polypeptide
 CC sequence (S2). Also included are: (1) an antibody or its portion that
 CC competitively inhibits the specific binding of (I) by at least 50 or
 CC 90 %; (2) a nucleic acid encoding the antibody (I) (or its single chain);
 CC (3) a vector comprising the nucleic acid; (4) a host cell comprising
 CC the nucleic acid or vector; and (5) a hybridoma producing the antibody.
 CC The antibody is useful for treating disease or disorder such as
 CC autoimmune diseases, systemic lupus erythematosus, rheumatoid arthritis,
 CC Sjogren's syndrome, cancer, preferably B cell cancer, chronic lymphocytic
 CC leukaemia, multiple myeloma, Hodgkin's lymphoma and non-Hodgkin's
 CC lymphoma, an immunodeficiency, hypo or hypergammaglobulinaemia,
 CC rheumatic heart disease, diabetes mellitus, autoimmune thyroiditis,
 CC Goodpasture's syndrome, Graves' disease, myasthenia gravis, autoimmune
 CC haemolytic anaemia, infertility, chronic active hepatitis, primary
 CC biliary cirrhosis, other disorders such as inflammatory skin diseases
 CC including psoriasis, allergic conditions, atherosclerosis, antigen-

CC antibody complex mediated diseases and autoimmune thrombocytopaenia. The
 CC antibody is also useful for diagnosing the disease or disorder, by
 CC assaying expression of Neutrokin- α and APRIL expression level, in
 CC cells or body fluid of an individual and comparing the levels with a
 CC standard expression level, where an increase or decrease in the assayed
 CC Neutrokin- α and APRIL expression level compared to the standard
 CC expression level is indicative of a disease or disorder. The antibody is
 CC also useful for reducing or stimulating immunoglobulin production and to
 CC inhibit or stimulate proliferation of a cell of haematopoietic origin,
 CC preferably a B cell. The gene for Neutrokin- α is located on
 CC chromosome 13q34. The present sequence is a non-human Neutrokin- α
 CC protein.

XX Sequence 309 AA;
 XX
 XX Query Match 91.7%; Score 1103.5; DB 23; Length 309;
 XX Best Local Similarity 74.4%; Pred. No. 3.2e-116; Mismatches 2; Indels 77; Gaps 5;
 XX Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;
 QY 1 MDESATLPPPCLCFCSEKGEKMGVYDPIITPQKEGA-----VLLSS 43
 DB 1 MDESATLPPPCLCFCSEKGEKMGVYDPIITPQKEGAFGICRDRLLAATLLALLSS 60
 QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLTPAAPRPHNSR 94
 DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
 QY 95 GHRNRAPFGPEETEEDVDLSAPPA-----LRNIQDCLLIADSDTP 137
 DB 121 GHRNRAPFGPEETEEDVDLSAPPAFCPLGCRHSQHDNDGMNLRNIQDCLLIADSDTP 180
 QY 138 TIRKGTYYFVFWLLSFKRGNAL-----YSQVLYTDFIFAMGHVIQK 180
 DB 181 TIRKGTYYFVFWLLSFKRGNALEKENKIVRQTGYFFIYSQVLYTDFIFAMGHVIQK 240
 QY 181 VHVFGDELSTLTLFRICQN-----LEEGDEIQALAI PRENAQISRNGDD 223
 DB 241 VHVFGDELSTLTLFRICQNMPKTLPNNSCYSAGIARLEEGDEIQALAI PRENAQISRNGDD 300
 QY 224 TFFGALKLL 232
 DB 301 TFFGALKLL 309

RESULT 3
 ABJ00717 ID ABJ00717 standard; Protein; 309 AA.

XX AC ABJ00717;

XX DT 05-SEP-2002 (first entry)

XX DE Murine B lymphocyte stimulator protein #1.

XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
 KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
 KW antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX OS Mus sp.

XX PN WO200216411-A2.

XX PD 28-FEB-2002.

XX PF 17-AUG-2001; 2001WO-US25850.

XX PR 18-AUG-2000; 2000US-226700P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;

XX DR WPI; 2002-499775/53.

XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B lymphocyte stimulator binding polypeptide -

XX PS Disclosure; Page 304-306; 387pp; English.

XX The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production; B cell proliferation
 CC and graft rejection involving administration of Blys binding polypeptide.
 CC The Blys binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein.

XX SQ Sequence 309 AA;

XX Query Match 91.7%; Score 1103.5; DB 23; Length 309;

XX Best Local Similarity 74.4%; Pred. No. 3.2e-116;

XX Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;

QY 1 MDESATLPPPCLCFCSEKGEKMGVYDPIITPQKEGA-----VLLSS 43

DB 1 MDESATLPPPCLCFCSEKGEKMGVYDPIITPQKEGAFGICRDRLLAATLLALLSS 60

QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLTPAAPRPHNSR 94

DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120

QY 95 GHRNRAPFGPEETEEDVDLSAPPA-----LRNIQDCLLIADSDTP 137

DB 121 GHRNRAPFGPEETEEDVDLSAPPAFCPLGCRHSQHDNDGMNLRNIQDCLLIADSDTP 180

QY 138 TIRKGTYYFVFWLLSFKRGNAL-----YSQVLYTDFIFAMGHVIQK 180

DB 181 TIRKGTYYFVFWLLSFKRGNALEKENKIVRQTGYFFIYSQVLYTDFIFAMGHVIQK 240

QY 181 VHVFGDELSTLTLFRICQN-----LEEGDEIQALAI PRENAQISRNGDD 223

DB 241 VHVFGDELSTLTLFRICQNMPKTLPNNSCYSAGIARLEEGDEIQALAI PRENAQISRNGDD 300

QY 224 TFFGALKLL 232

DB 301 TFFGALKLL 309

RESULT 4

ABP47219 ID ABP47219 standard; Protein; 309 AA.

XX AC ABP47219;

XX DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv VH CDR3 SEQ ID 3230.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.
XX PN WO200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US19110.
XX PR 16-JUN-2000; 2000US-212210P.
XX PR 17-OCT-2000; 2000US-240816P.
XX PR 16-MAR-2001; 2001US-276248P.
XX PR 21-MAR-2001; 2001US-277379P.
XX PR 25-MAY-2001; 2001US-293499P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX Disclosure; Page 3140-3141; 3148pp; English.
XX This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method
XX of the invention.
XX SQ Sequence 309 AA;
Query Match 91.7%; Score 1103.5; DB 23; Length 309;
Best Local Similarity 74.4%; Pred. No. 3.2e-116;
Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;
QY 1 MDESAKTLPPCLCFCEKSGEDMKVGYDPTTPQKEGA-----VLLSS 43
DB 1 MDESAKTLPPCLCFCEKSGEDMKVGYDPTTPQKEGAFCRDRGRLLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLMNLRMELQSYRGSAAPAAA-----KLTTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLMNLRMELQSYRGSAAPAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRRAPFGPEETEQQDVLSDAPPA-----LRNIIDCQLIADSDTP 137
DB 121 GHRNRRAPFGPEETEQQDVLSDAPPAAPCLPGCRHSQHDNDGNNLRNIIQDCLLIADSDTP 180
QY 138 TIRKGTTFVFWLLSKFKGNAL-----YSQVLYTDFPFAMGHVIOQRK 180
DB 181 TIRKGTTFVFWLLSKFKGNAL-----YSQVLYTDFPFAMGHVIOQRK 240
QY 181 VHVFGDELSLVTLPFCION-----LEEDEIQLAIPRENAQISRNGDD 223
DB 241 VHVFGDELSLVTLPFCIONMPTLNNCSYSGIARLEEGDEIQLAIPRENAQISRNGDD 300
QY 224 TFFGALKLL 232
|||||

DB 301 TFFGALKLL 309
RESULT 5
ABG33578
ID ABG33578 standard; Protein; 309 AA.
XX AC ABG33578;
XX DT 15-JUL-2002 (first entry)
XX DE Murine B Lymphocyte Stimulator (Blys) protein #1.
XX KW B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide;
XX KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
XX KW synovial fluid; saliva; mucus; mouse.
XX OS Mus sp.
XX PN WO200216412-A2.
XX PD 28-FEB-2002.
XX PF 17-AUG-2001; 2001WO-US25891.
XX PR 18-AUG-2000; 2000US-226489P.
XX (DYAX-) DYAX CORP.
XX Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
XX WPI; 2002-351647/38.
XX New B-lymphocyte stimulator binding polypeptide useful in detecting or
XX isolating Blys or Blys-like polypeptide comprises a specified amino
XX acid sequence -
XX Disclosure; Page 186-188; 269pp; English.
XX The invention relates to a B Lymphocyte Stimulator (Blys) binding
XX polypeptide. Blys binding peptides bind Blys or Blys-like proteins
XX reversibly or irreversibly. The binding peptides are used in detection,
XX isolation and/or purification of Blys in a solution such as water or a
XX buffer solution, as well as any fluid and/or cell obtained from an
XX individual biological fluid, body tissue, body cell, cell line, tissue
XX culture or other source containing Blys or Blys-like polypeptides. The
XX biological fluids include sera, plasma, lymph, blood, blood fraction,
XX urine, synovial fluid, spinal fluid, saliva and mucus. Sequences
XX ABG33578 and ABG33579 represent murine B Lymphocyte Stimulator proteins.
XX SQ Sequence 309 AA;
Query Match 91.7%; Score 1103.5; DB 23; Length 309;
Best Local Similarity 74.4%; Pred. No. 3.2e-116;
Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;
QY 1 MDESAKTLPPCLCFCEKSGEDMKVGYDPTTPQKEGA-----VLLSS 43
DB 1 MDESAKTLPPCLCFCEKSGEDMKVGYDPTTPQKEGAFCRDRGRLLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLMNLRMELQSYRGSAAPAAA-----KLTTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLMNLRMELQSYRGSAAPAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRRAPFGPEETEQQDVLSDAPPA-----LRNIIDCQLIADSDTP 137
DB 121 GHRNRRAPFGPEETEQQDVLSDAPPAAPCLPGCRHSQHDNDGNNLRNIIQDCLLIADSDTP 180
QY 138 TIRKGTTFVFWLLSKFKGNAL-----YSQVLYTDFPFAMGHVIOQRK 180
DB 181 TIRKGTTFVFWLLSKFKGNAL-----YSQVLYTDFPFAMGHVIOQRK 240
QY 181 VHVFGDELSLVTLPFCION-----LEEDEIQLAIPRENAQISRNGDD 223

Db 241 VHVFGDELSVTLFRCIQNMPTLPNNSCYSAGIARLEEGDEIQAIAPRENAQISRNGDD 300
 QY 224 TFFGALKLL 232
 Db 301 TFFGALKLL 309

RESULT 6
 AAU79147
 ID AAU79147 standard; Protein; 309 AA.
 AC AAU79147;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Mouse Neutrokin-alpha-like protein fragment #1.
 XX
 KW Mouse; Neutrokin-alpha-like; antibody; immunogen; B-cell cancer;
 autoimmune disease; Sjogren's syndrome; systemic lupus erythematosus;
 rheumatoid arthritis; chronic lymphocytic leukaemia; multiple myeloma;
 Hodgkin's lymphoma; non-Hodgkin's lymphoma; hypergammaglobulinemia;
 APRIL; a proliferation-inducing ligand.
 KW
 XX
 OS Mus musculus.
 XX
 PN WO200218620-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 15-AUG-2001; 2001WO-US25549.
 XX
 PR 15-AUG-2000; 2000US-225628P.
 PR 23-AUG-2000; 2000US-227008P.
 PR 22-SEP-2000; 2000US-234338P.
 PR 17-OCT-2000; 2000US-240806P.
 PR 30-NOV-2000; 2000US-250020P.
 PR 06-MAR-2001; 2001US-276248P.
 PR 25-MAY-2001; 2001US-293499P.
 PR 07-JUN-2001; 2001US-296122P.
 PR 13-JUL-2001; 2001US-304809P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Yu G, Ebner R, Ni J, Rosen CA, Ullrich S;
 XX
 XX WPI; 2002-304259/34.
 DR
 XX
 PT An isolated antibody or portion that specifically binds to a protein
 useful in the treatment of diseases such as hypergammaglobulinemia and
 cancer.
 PT
 XX
 PS Disclosure; Page 476-477; 482pp; English.
 XX
 CC The present invention relates to a new antibody, or portion, that
 specifically binds to a protein which has a 285 or 250 amino acid
 sequence as fully defined in the specification. The antibody of the
 CC invention is useful in treating a disease or disorder such as cancer,
 CC especially B-cell cancer, autoimmune diseases such as Sjogren's
 CC syndrome, systemic lupus erythematosus, rheumatoid arthritis, chronic
 CC lymphocytic leukaemia, multiple myeloma, Hodgkin's lymphoma,
 CC non-Hodgkin's lymphoma or hypergammaglobulinemia, or in diagnosing a
 CC disease or disorder comprising assaying expression of Neutrokin-alpha
 CC and APRIL (a proliferation-inducing ligand) in cells or body fluids using
 CC antibodies and comparing the Neutrokin-alpha and APRIL expression level
 CC with a standard Neutrokin-alpha and APRIL expression level, whereby an
 CC increase or decrease in the assayed Neutrokin-alpha and APRIL expression
 CC level compared to the standard levels is indicative of a disease or
 CC disorder. The present amino acid sequence represents the mouse
 CC Neutrokin-alpha-like protein fragment #1.
 XX
 SQ Sequence 309 AA;

Query Match 91.7%; Score 1103.5; DB 23; Length 309;
 Best Local Similarity 74.4%; Pred. No. 3.2e-116;
 Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;

QY 1 MDESAKTLPPPCICFCSEKGEDMKVGYDPIITPOKEEGR-----VLLSS 43
 Db 1 MDESAKTLPPPCICFCSEKGEDMKVGYDPIITPOKEEGR-----VLLSS 60
 QY 44 SFTAMSLYQLAALQADLMNLRMELQSYRGSAATPAAAGAPELTAGVKLTTPAARPHNSR 94
 Db 61 SFTAMSLYQLAALQADLMNLRMELQSYRGSAATPAAAGAPELTAGVKLTTPAARPHNSR 120
 QY 95 GHRNRRAFPGPETEEDVDLSAPPA-----LRNIQDCQLIADSDTP 137
 Db 121 GHRNRRAFPGPETEEDVDLSAPPA-----LRNIQDCQLIADSDTP 180
 QY 138 TIRKGTTFVFWLLSFKEGNAL-----YSQVLYTDFIFANGHVIORCK 180
 Db 181 TIRKGTTFVFWLLSFKEGNAL-----YSQVLYTDFIFANGHVIORCK 240
 QY 181 VHVFGDELSVTLFRCIQNMPTLPNNSCYSAGIARLEEGDEIQAIAPRENAQISRNGDD 223
 Db 241 VHVFGDELSVTLFRCIQNMPTLPNNSCYSAGIARLEEGDEIQAIAPRENAQISRNGDD 300
 QY 224 TFFGALKLL 232
 Db 301 TFFGALKLL 309

RESULT 7
 AAU10943
 ID AAU10943 standard; Protein; 309 AA.
 AC AAU10943;
 DT 12-MAR-2002 (first entry)
 XX
 DE Mouse AGP-3.
 XX
 KW Mouse; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
 dermatological; neuroprotective; nontropic; immunomodulator; metabolic;
 KW analgesic; analgesic; nephrotropic; osteopathic; cytostatic; fever;
 KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;
 KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;
 KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
 KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
 KW pancreatitis; amyotrophic lateral sclerosis; AIDS; Alzheimer's disease;
 KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
 KW multiple sclerosis; Parkinson's disease; transgenic animal.
 XX
 OS Mus musculus.
 XX
 PN WO200185782-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 12-FEB-2001; 2001WO-US04568.
 XX
 PR 11-FEB-2000; 2000US-181800P.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Hsu H;
 XX
 XX WPI; 2002-049441/06.
 DR N-PSDB; AAS18545.
 XX
 PT Composition, useful for identifying modulator of receptor for treating
 asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor
 PT ligand family member) receptor and encoding nucleic acids -
 XX
 PS Disclosure; Fig 2; 124pp; English.
 XX

CC The invention relates to a composition (I) comprising AGP-3 receptor
 CC (tumour necrosis factor ligand family member) related protein (II)
 CC attached to a vehicle protein. (I) is useful for modulating AGP-3-related
 CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
 CC assays to identify cells and tissues that express AGP-3R or proteins
 CC related to AGP-3R-related protein and for identifying compounds
 CC (agonists or antagonists) that interact with AGP-3R proteins. (II) is
 CC also useful for identifying intracellular proteins that interact with
 CC the respective cytoplasmic domains by yeast two-hybrid screening
 CC process. (II) is involved in B cell growth, survival and activation
 CC particularly in lymph node, spleen, and Peyer's patches. AGP-3R
 CC agonists and antagonists identified using (II) are used for modulating
 CC B cell response and are used to treat diseases characterised by
 CC inflammatory processes or deregulated immune response such as
 CC rheumatoid arthritis, graft-versus-host disease, Crohn's disease,
 CC lupus, etc. (II) is also useful in the production of hybridoma cells
 CC which are derived from B cells, which involves treating the hybridoma
 CC cells with (II). (II) is useful in the treatment of inflammatory
 CC conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc.
 CC (II), its agonists or antagonists are useful for treating acute
 CC pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
 CC asthma, atherosclerosis, cachexia/anorexia, diabetes, fever,
 CC glomerulonephritis, inflammatory bowel disease, ischaemic injury
 CC including cerebral ischaemia, multiple myeloma, multiple sclerosis,
 CC osteoporosis, Parkinson's disease, pain, reperfusion injury, septic
 CC shock, etc. The nucleic acids are also useful for developing transgenic
 CC animals expressing (II), which are useful for producing the polypeptides
 CC and for the study of in vivo biological activity. The present
 CC sequence represents the amino acid sequence of mouse AGP-3.

XX Sequence 309 AA;

Query Match 91.7%; Score 1103.5; DB 23; Length 309;
 Best Local Similarity 74.4%; Pred. No. 3.2e-116; Indels 77; Gaps 5;
 Matches 230; Conservative 0; Mismatches 2;

QY 1 MDESAKTLPPPCLCFCSEKGDGMKGYDPIPTPQKEEGA-----VLSS 43
 DB 1 MDESAKTLPPPCLCFCSEKGDGMKGYDPIPTPQKEGAWFGICRDGRLLAATLLALLSS 60

QY 44 SFTAMSLYQLAALQADLMLNLMELQSYRGSATPAAA-----KLITPAAPRPHNSR 94
 DB 61 SFTAMSLYQLAALQADLMLNLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120

QY 95 GHRNRAFPQPEETQDDVLSAPPA-----LRNIQDCLQLADSDTP 137
 DB 121 GHRNRAFPQPEETQDDVLSAPPAFLPGRHSQDDNGMNLNIIQDCLQLADSDTP 180

QY 138 TIRKGTTFVFWLLSFKRGNAL-----YSQVLYTDFIFANGHVIQRKK 180
 DB 181 TIRKGTTFVFWLLSFKRGNALEKENIVVQTGYFYISQVLYTDFIFANGHVIQRKK 240

QY 181 VHVFGDELSTVTLFRCIQN-----LREGDEIQLAIPRENAQISRNGDD 223
 DB 241 VHVFGDELSTVTLFRCIQNMPKTPNNSCYLAGIARLEGEDEIQLAIPRENAQISRNGDD 300

QY 224 TFFGALKLL 232
 DB 301 TFFGALKLL 309

RESULT 8

AAB08262

ID AAB08262 standard; Protein; 309 AA.

XX

AC AAB08262;

XX 04-DEC-2000 (first entry)

DT

XX Amino acid sequence of a murine AGP-3 polypeptide.

XX AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;

KW type II transmembrane protein; B cell stimulatory factor;

KW inflammatory disorder; immune disorder; rheumatoid arthritis;
 lupus and graft versus host disease.

XX Mus sp.

XX Key Location/Qualifiers
 FH Domain 1..47 /note= "intracellular domain"
 FT Region 48..73 /note= "transmembrane region"
 FT Domain 74..309 /note= "extracellular domain"
 FT Misc-difference 106 /note= "unspecified amino acid encoded by AAA"
 FT Misc-difference 271 /note= "Ser encoded by TTG"
 FT Misc-difference 282 /note= "Glu encoded by GG"
 FT Misc-difference 295 /note= "Ser encoded by CAC"
 FT Misc-difference 296 /note= "Arg encoded by GC"

XX WO2000047740-A2.

XX 17-AUG-2000.

XX 11-FEB-2000; 2000WO-US03653.

XX 12-FEB-1999; 99US-0119906.

XX 18-NOV-1999; 99US-0166271.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Hsu H;

XX WPI; 2000-558217/51.

XX N-PSDB; AAA63942.

XX Novel polypeptides comprising tumour necrosis factor ligand family
 proteins, useful for treating inflammatory and immune disorders, e.g.
 rheumatoid arthritis -

XX Claim 4; Fig 2; 71pp; English.

XX The present sequence encodes a murine AGP-3 polypeptide. AGP-3 is a
 CC tumour necrosis factor (TNF) ligand family member. AGP-3 is a type II
 CC transmembrane protein, and is a potent B cell stimulatory factor.
 CC Expression of AGP-3 correlates to increases in the number of B cells
 CC and immunoglobulins produced. AGP-3 proteins, antibodies, and nucleic
 CC acids may be used to treat inflammatory and immune disorders,
 CC e.g. rheumatoid arthritis, Crohn's disease, lupus and graft versus
 CC host disease. The nucleic acids may be used to regulate the expression
 CC of an AGP-3 related protein. The AGP-3 proteins, antibodies and nucleic
 CC acids are also useful for the detection of AGP-3 agonists, antagonists
 CC and characterizing interactions with AGP-3 related proteins.
 CC note: this sequence is not specifically claimed. It is only mentioned
 CC in the claims, in that a polypeptide that does not comprise the present
 CC sequence is claimed.

XX Sequence 309 AA;

Query Match 91.2%; Score 1097.5; DB 21; Length 309;
 Best Local Similarity 74.1%; Pred. No. 1.6e-115; Indels 77; Gaps 5;
 Matches 229; Conservative 0; Mismatches 3;

QY 1 MDESAKTLPPPCLCFCSEKGDGMKGYDPIPTPQKEEGA-----VLSS 43
 DB 1 MDESAKTLPPPCLCFCSEKGDGMKGYDPIPTPQKEGAWFGICRDGRLLAATLLALLSS 60

QY 44 SFTAMSLYQLAALQADLMLNLMELQSYRGSATPAAA-----KLITPAAPRPHNSR 94
 DB 61 SFTAMSLYQLAALQADLMLNLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120

QY 95 GHRNRAPPGPEETEODVLSAPPA-----LRNIQDCLQIADSDTP 137
 |||||
 Db 121 GHRNRAPPGPEETEODVLSAPPA-----LRNIQDCLQIADSDTP 180
 |||||
 QY 138 TIRKGTYYTFVPMWLLSFKRGNAL-----YSQVLYTDFPFAMGHVIOQKK 180
 |||||
 Db 181 TIRKGTYYTFVPMWLLSFKRGNAL-----YSQVLYTDFPFAMGHVIOQKK 240
 |||||
 QY 181 VHVFGDELSLVTLFRCIQ-----LEEGDEIQIAIPRENAQISRNGDD 223
 |||||
 Db 241 VHVFGDELSLVTLFRCIQ-----LEEGDEIQIAIPRENAQISRNGDD 300
 |||||
 QY 224 TFFGALKUL 232
 |||||
 Db 301 TFFGALKUL 309
 |||||

RESULT 9
 AAY04393
 ID AAY04393 standard; Protein; 290 AA.

XX AC AAY04393;

DT 24-JUN-1999 (first entry)

DE Murine Kay-ligand.

KW Kay-ligand; tumour necrosis factor family; TNF; immune system;
 KW cytokine; autoimmune disease; tissue graft; cancer; cell death.

XX OS Mus sp.

PN WO9912964-A2.

XX PD 18-MAR-1999.

XX PF 11-SEP-1998; 98WO-US19037.

XX PR 12-SEP-1997; 97US-0058786.

XX PA (BIOJ) BIOGEN INC.

XX PI Tschopp J;

XX DR WPI; 1999-243715/20.

XX DR N-PSDB; AAX33331.

XX PT New human or murine Kay-ligands, members of the tumour necrosis
 PT factor family

XX PS Claim 12; Page 33; 41pp; English.

XX The present sequence represents murine Kay-ligand, which is a member of
 the tumour necrosis factor (TNF) family of cytokines. Pharmaceutical
 compositions containing the Kay-ligand can be used to suppress or
 stimulate the immune system, especially to prevent or reduce the
 severity of autoimmune diseases or response to a tissue graft or to
 treat cancer. An agent capable of interfering with the Kay-ligand can be
 used to induce cell death. The Kay-ligand can also be used to identify
 its receptors.

XX SQ Sequence 290 AA;

Query Match 83.0%; Score 999; DB 20; Length 290;

Best Local Similarity 71.9%; Pred. No. 2.1e-104;

Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESAKTLPPPCLCFCSEKGMKVGYPITPQKEGA-----VLSS 43

Db 1 MDESAKTLPPPCLCFCSEKGMKVGYPITPQKEGA-----VLSS 60

QY 44 SFTMSLYQLAALQADLNLRLMELQSYRGSAATPAAA-----KLLTPAARPHNSR 94

Db 61 SFTMSLYQLAALQADLNLRLMELQSYRGSAATPAAAAGAPELTAGVKLLTPAARPHNSR 120
 |||||
 QY 95 GHRNRAPPGPEETEODVLSAPPA-----LRNIQDCLQIADSDTP 154
 |||||
 Db 121 GHRNRAPPGPEETEODVLSAPPA-----LRNIQDCLQIADSDTP 178
 |||||
 QY 155 RGNAL-----YSQVLYTDFPFAMGHVIOQKKVHVFGEDELSTLFRCI 197
 |||||
 Db 179 RGNALEEKENKIVVRQTGYFFIYSQVLYTDFPFAMGHVIOQKKVHVFGEDELSTLFRCI 238
 |||||
 QY 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKUL 232
 |||||
 Db 239 QNPKTLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKUL 290
 |||||

RESULT 10

AAW93587

ID AAW93587 standard; Protein; 290 AA.

XX AC AAW93587;

DT 18-JUN-1999 (first entry)

DE Mouse TNRL1-alpha protein.

KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
 KW developmental abnormality; gestational abnormality; prostate cancer;
 KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
 KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
 KW apoptosis; mouse; TNRL1-alpha.

XX OS Mus sp.

PN WO9911791-A2.

XX PD 11-MAR-1999.

XX PF 04-SEP-1998; 98WO-US18393.

XX PR 05-SEP-1997; 97US-0924634.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Chaudhary PM;

XX DR WPI; 1999-205191/17.

XX DR N-PSDB; AAX23421.

XX New Tumour Necrosis Factor family receptor polypeptides and ligands -
 useful for diagnosis and treatment of prostate cancer and
 developmental or gestational abnormalities

XX Claim 34; Fig 11B; 156pp; English.

XX This invention describes isolated Tumour Necrosis Factor (TNF) family
 receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
 fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
 their active fragments. APO4 is useful for diagnosing prostate cancer
 by determining levels of APO4 in an individual. Prostate cancer can also
 be treated using APO4 selective binding agents linked to a therapeutic
 moiety. APO4 polypeptides are also useful for identifying selective
 binding agents, useful in diagnosis/treatment of disease by binding of
 agents to the polypeptide/active fragment which is extracellular, or
 expressed on the cell surface. The binding is preferably performed in
 vivo. APO4 polypeptides/active fragments are also useful for screening
 for agonists and antagonists by binding and observing the change in APO4
 activity. Effective pharmacological agents useful in diagnosis or
 treatment of disease are also identified using APO4 polypeptides/active
 fragments and APO4 signal transducer molecules that specifically interact
 with a cytoplasmic domain of APO4 and detecting a change in level of APO4
 activity. The method is performed in vivo or in vitro. APO polypeptides
 are all useful as immunogens for preparing antibodies. APO4 is also

CC useful for diagnosis/treatment of developmental or gestational
 CC abnormalities. APO8 was transfected to human breast carcinoma cell line
 CC MCF-7, and induced apoptosis.

XX SQ Sequence 290 AA;

Query Match 83.0%; Score 999; DB 20; Length 290;
 Best Local Similarity 71.9%; Pred. No. 2.1e-104;
 Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESATLPPCLCFCEKEDMKVGYDPTTPQKEGA-----VLLSS 43
 DB 1 MDESATLPPCLCFCEKEDMKVGYDPTTPQKEGAWFGICRDRLLAATLLALLSS 60

QY 44 SFTAMSLYQLAALQADLMNLRMELQSYRGSGATPAAA-----KLLTPAAPRPHNSR 94
 DB 61 SFTAMSLYQLAALQADLMNLRMELQSYRGSGATPAAAGAPELTAGVKLLTPAAPRPHNSR 120

QY 95 GHRNRAPFGPEETEEDVDLSAPPALRNIIODCLQIADSDPTPIRKGTYYTFVFWLLSFK 154
 DB 121 GHRNRAPFGPEETEEDVDLSAPPA--PCLPGCRHSQHDNDGMNLRNRTYTFVFWLLSFK 178

QY 155 RGNAL-----YSQVLYTDPFAMGHVIOQRKVVHFGDELSTLTPRCI 197
 DB 179 RGNALKEENKIVVRQGTGYFYISQVLYTDPFAMGHVIOQRKVVHFGDELSTLTPRCI 238

QY 198 QN-----LEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 232
 DB 239 QNMPKTLNNSCYSAGIARLEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 290

RESULT 11
 ID AAE07880
 AC AAE07880;
 DT 01-NOV-2001 (first entry)
 DE Mouse BAFF protein.

KW Mouse; tumour necrosis factor; TNF; APBF; APRIL; BAFF; therapy; melanoma;
 KW immune system-related disorder; cancer; renal cell; breast; stomach;
 KW rectal; colon; throat; bladder; ovarian carcinoma; cellular disorder;
 KW gastrointestinal; scleroderma; Kaposi's sarcoma; chronic leukaemia;
 KW squamous cell carcinoma; hyperproliferative condition; pannus formation;
 KW rheumatoid arthritis; postsurgical scarring; fibrosis; liver; uterine;
 KW lung; immunodeficiency; inflammatory disease; lymphadenopathy; vulnary;
 KW autoimmune disease; graft versus host disease; dermatological;
 KW antiinflammatory; immunosuppressive; cytostatic.

OS Mus sp.
 XX WO200158949-A2.
 XX 16-AUG-2001.
 XX 08-FEB-2001; 2001WO-US04121.
 XX 11-FEB-2000; 2000US-0181670.
 XX (BIOJ) BIOGEN INC.
 XX Rennert PD, Thompson JS, Ambrose C, Cachero TG;
 XX WPI; 2001-514644/56.
 XX N-PSDB; AAD14418.
 XX New heteromeric ligand of tumor necrosis factor (TNF) family, useful
 PT for diagnosis, treatment of immune system-related disorders in humans,
 PT comprises TNF-family member APRIL subunit linked non-covalently to
 PT TNF-family member BAFF subunit -

PS Claim 2; Fig 2d; 42pp; English.

XX The present invention relates to an isolated heteromeric ligand of
 CC tumour necrosis factor (TNF)-family, referred to as APBF comprising a
 CC TNF-family member APRIL subunit linked non-covalently to TNF-family
 CC member BAFF subunit. APBF is useful for diagnosis or treatment of
 CC various immune system-related disorders in mammals, preferably humans.
 CC Such disorders include cancer, including cellular disorders, for e.g.
 CC renal cell cancer, Kaposi's sarcoma, chronic leukaemia, breast cancer,
 CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma,
 CC colon cancer, bladder cancer, squamous cell carcinoma and
 CC gastrointestinal or stomach cancer, cellular hyperproliferative
 CC conditions, such as scleroderma, pannus formation in rheumatoid
 CC arthritis, postsurgical scarring and lung, liver and uterine fibrosis
 CC and immunodeficiencies, inflammatory diseases, lymphadenopathy,
 CC autoimmune diseases and graft versus host disease. APBF is also useful
 CC for producing monoclonal or polyclonal antibodies and for identifying
 CC novel modulators affecting biological function and receptors interacting
 CC with APBF. The present sequence is mouse BAFF protein.

XX SQ Sequence 290 AA;

Query Match 83.0%; Score 999; DB 22; Length 290;
 Best Local Similarity 71.9%; Pred. No. 2.1e-104;
 Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESATLPPCLCFCEKEDMKVGYDPTTPQKEGA-----VLLSS 43
 DB 1 MDESATLPPCLCFCEKEDMKVGYDPTTPQKEGAWFGICRDRLLAATLLALLSS 60

QY 44 SFTAMSLYQLAALQADLMNLRMELQSYRGSGATPAAA-----KLLTPAAPRPHNSR 94
 DB 61 SFTAMSLYQLAALQADLMNLRMELQSYRGSGATPAAAGAPELTAGVKLLTPAAPRPHNSR 120

QY 95 GHRNRAPFGPEETEEDVDLSAPPALRNIIODCLQIADSDPTPIRKGTYYTFVFWLLSFK 154
 DB 121 GHRNRAPFGPEETEEDVDLSAPPA--PCLPGCRHSQHDNDGMNLRNRTYTFVFWLLSFK 178

QY 155 RGNAL-----YSQVLYTDPFAMGHVIOQRKVVHFGDELSTLTPRCI 197
 DB 179 RGNALKEENKIVVRQGTGYFYISQVLYTDPFAMGHVIOQRKVVHFGDELSTLTPRCI 238

QY 198 QN-----LEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 232
 DB 239 QNMPKTLNNSCYSAGIARLEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 290

RESULT 12
 ID ABG96470
 AC ABG96470;
 DT 11-DEC-2002 (first entry)
 DE Mouse Neutrokin-alpha-like protein fragment #3.

KW Neutrokin-alpha; cytokine; autoimmune disease; cancer;
 KW systemic lupus erythematosus; rheumatoid arthritis; Sjogren's syndrome;
 KW B cell cancer; chronic lymphocytic leukaemia; multiple myeloma;
 KW Hodgkin's lymphoma; non-Hodgkin's lymphoma; immunodeficiency;
 KW hypergammaglobulinaemia; hypogammaglobulinaemia; rheumatic heart disease;
 KW diabetes mellitus; autoimmune thyroiditis; Goodpasture's syndrome;
 KW Graves' disease; myasthenia gravis; autoimmune haemolytic anaemia;
 KW infertility; chronic active hepatitis; primary biliary cirrhosis;
 KW inflammatory skin disease; psoriasis; allergy; atherosclerosis;
 KW autoimmune thrombocytopaenia; antibody; chromosome 13q34.

OS Mus musculus.
 XX US2002115112-A1.
 XX 22-AUG-2002.

CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of Blys binding polypeptide.
 CC The Blys binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of haematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hyperagmaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein.

XX Sequence 290 AA;

Query Match 83.0%; Score 999; DB 23; Length 290;
 Best Local Similarity 71.9%; Pred. No. 2.1e-104;
 Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGA-----VLSS 43
 |||||
 DB 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGA-----VLSS 60
 |||||

QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAA-----KLTPAAPRPHNSR 94
 |||||
 DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAAGAPELTAGVKLLTPAAPRPHNSR 120
 |||||

QY 95 GHRNRRAFPQPEETEQQVDLSAPPALRNIIQDCLQIADSDPTTKGTYTFVPWLLSPK 154
 |||||
 DB 121 GHRNRRAFPQPEETEQQVDLSAPPA--PCLPGCRHSQHDNGMNLNRNTYTFVPWLLSPK 178
 |||||

QY 155 RGNAL-----YSQVLYTDPIFAMGHVIOQRKKVHVFGEDELSTLTLFRCI 197
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 DB 179 RGNALKEENKIVVRQGTGYFFIYSQVLYTDPIFAMGHVIOQRKKVHVFGEDELSTLTLFRCI 238
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QY 198 QN-----LEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 232
 |||||
 DB 239 QNMPKTLPNNSCYSAGIARLEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 290
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RESULT 14
 ABP47220
 ID ABP47220 standard; Protein; 290 AA.
 AC ABP47220;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv VH CDR3 SEQ ID 3231.
 XX
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 FN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US19110.
 XX
 PR 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 DR WPI; 2002-114799/15.
 XX
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
 the diagnosis and treatment of cancers and immune disorders -
 XX Disclosure; Page 3141-3142; 3148pp; English.
 PS
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic, and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.

XX Sequence 290 AA;

Query Match 83.0%; Score 999; DB 23; Length 290;
 Best Local Similarity 71.9%; Pred. No. 2.1e-104;
 Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGA-----VLSS 43
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QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAA-----KLTPAAPRPHNSR 94
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QY 95 GHRNRRAFPQPEETEQQVDLSAPPALRNIIQDCLQIADSDPTTKGTYTFVPWLLSPK 154
 |||||
 DB 121 GHRNRRAFPQPEETEQQVDLSAPPA--PCLPGCRHSQHDNGMNLNRNTYTFVPWLLSPK 178
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QY 155 RGNAL-----YSQVLYTDPIFAMGHVIOQRKKVHVFGEDELSTLTLFRCI 197
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 DB 179 RGNALKEENKIVVRQGTGYFFIYSQVLYTDPIFAMGHVIOQRKKVHVFGEDELSTLTLFRCI 238
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QY 198 QN-----LEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 232
 |||||
 DB 239 QNMPKTLPNNSCYSAGIARLEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 290
 |||||

RESULT 15
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 ID ABG33579 standard; Protein; 290 AA.
 XX
 AC ABG33579;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Murine B Lymphocyte Stimulator (Blys) protein #2.
 XX
 KW B lymphocyte stimulator protein; B lymphocyte stimulator binding peptide;
 KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
 KW synovial fluid; saliva; mucus; mouse.
 XX
 OS Mus sp.
 XX
 FN WO200216412-A2.
 XX
 PD 28-FEB-2002.

XX 17-AUG-2001; 2001WO-US25891.
XX
XX
XX 18-AUG-2000; 2000US-226489P.
XX
XX (DYAX-) DYAX CORP.
XX
XX Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
XX
XX WPI; 2002-351647/38.
XX
XX New B-lymphocyte stimulator binding polypeptide useful in detecting or
PT isolating Blys or Blys-like polypeptide comprises a specified amino
PT acid sequence
XX
XX
PS Disclosure; Page 188-189; 269pp; English.
XX
XX The invention relates to a B Lymphocyte Stimulator (Blys) binding
CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins
CC reversibly or irreversibly. The binding peptides are used in detection,
CC isolation and/or purification of Blys in a solution such as water or a
CC buffer solution, as well as any fluid and/or cell obtained from an
CC individual biological fluid, body tissue, body cell, cell line, tissue
CC culture or other source containing Blys or Blys-like polypeptides. The
CC biological fluids include sera, plasma, lymph, blood, blood fraction,
CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences
CC ABG33578 and ABG33579 represent murine B Lymphocyte Stimulator proteins.
XX
SQ Sequence 290 AA;

Query Match 83.0%; Score 999; DB 23; Length 290;
Best Local Similarity 71.9%; Pred. No. 2.1e-104;
Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

Qy 1 MDESAKTLPPPCLCFCSEKEDMKVGYDPTTPQKEGA-----VLSS 43
Db 1 MDESAKTLPPPCLCFCSEKEDMKVGYDPTTPQKEGA-----VLSS 60
Qy 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSAATPAAA-----KLTPAAPRPHNSR 94
Db 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSAATPAAAAGAPDELTAGVKLLTPAAPRPHNSR 120
Qy 95 GHRNRRAPFGPEETEQQDVLDSAPPALRNIIQCLQLIADSDPTTIRKGYTFVPWLLSFK 154
Db 121 GHRNRRAPFGPEETEQQDVLDSAPPA--PCLPCRHSQHDDNGMNLNRNTYTFVPWLLSFK 178
Qy 155 RGNAL-----YSQVLYTDPPIFAMGHVIOQKKVHVFGEDELSTLTLFRCI 197
Db 179 RGNALEEKENKIVVRQTYGYFYISQVLYTDPPIFAMGHVIOQKKVHVFGEDELSTLTLFRCI 238
Qy 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 232
Db 239 QNMPTLNNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 290

Search completed: February 3, 2004, 07:48:17
Job time : 39.6667 secs

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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:45:42 ; Search time 224.782 Seconds
(without alignments)
216.106 Million cell updates/sec

Title: US-09-911-777-2

Perfect score: 1204

Sequence: 1 MDESAKTLPPCLFCSEKSG.....ENAIQSRNGDDTFFGALKLL 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1204	100.0	232	15	US-10-045-574A-2
3	1103.5	91.7	309	10	US-09-929-493-39
4	1103.5	91.7	309	10	US-09-779-050A-4
5	1103.5	91.7	309	11	US-09-880-748-3230
6	1103.5	91.7	309	11	US-09-932-613-175
7	1103.5	91.7	309	12	US-10-270-487-39
8	1103.5	91.7	309	12	US-09-932-322-175
9	999	83.0	290	10	US-09-929-493-40
10	999	83.0	290	11	US-09-880-748-3231
11	999	83.0	290	11	US-09-932-613-176
12	999	83.0	290	12	US-10-270-487-40
13	999	83.0	290	12	US-09-932-322-176
14	999	83.0	290	15	US-10-214-065-8
15	992.5	82.4	289	10	US-09-929-493-38

16	992.5	82.4	289	12	US-10-270-487-38	Sequence 38, Appl
17	780.5	64.8	239	11	US-09-880-748-3232	Sequence 3232, Ap
18	780.5	64.8	239	11	US-09-932-613-177	Sequence 177, App
19	780.5	64.8	239	12	US-09-932-322-177	Sequence 177, App
20	723.5	60.1	207	11	US-09-880-748-3234	Sequence 3234, Ap
21	723.5	60.1	207	11	US-09-932-613-179	Sequence 179, App
22	723.5	60.1	207	12	US-09-932-322-179	Sequence 179, App
23	696	57.8	218	9	US-09-911-777-1	Sequence 1, Appli
24	681	56.6	220	15	US-10-045-574A-1	Sequence 1, Appli
25	681	56.6	220	11	US-09-880-748-3233	Sequence 3233, Ap
26	681	56.6	220	11	US-09-932-613-178	Sequence 178, App
27	681	56.6	220	12	US-09-932-322-178	Sequence 178, App
28	625	51.9	188	11	US-09-880-748-3235	Sequence 3235, Ap
29	625	51.9	188	11	US-09-932-613-180	Sequence 180, App
30	625	51.9	188	12	US-09-932-322-180	Sequence 180, App
31	622.5	51.7	285	8	US-08-971-317A-2	Sequence 2, Appli
32	622.5	51.7	285	9	US-09-193-663-2	Sequence 2, Appli
33	622.5	51.7	285	9	US-09-877-156-1	Sequence 1, Appli
34	622.5	51.7	285	9	US-09-879-919-23	Sequence 23, Appl
35	622.5	51.7	285	10	US-09-929-493-2	Sequence 2, Appli
36	622.5	51.7	285	10	US-09-779-050A-2	Sequence 2, Appli
37	622.5	51.7	285	11	US-09-302-863-4	Sequence 4, Appli
38	622.5	51.7	285	11	US-09-880-748-3228	Sequence 3228, Ap
39	622.5	51.7	285	11	US-09-932-613-173	Sequence 173, App
40	622.5	51.7	285	12	US-10-137-870-24	Sequence 24, Appl
41	622.5	51.7	285	12	US-10-140-018-24	Sequence 24, Appl
42	622.5	51.7	285	12	US-10-140-021-24	Sequence 24, Appl
43	622.5	51.7	285	12	US-10-140-274-24	Sequence 24, Appl
44	622.5	51.7	285	12	US-10-140-471-24	Sequence 24, Appl
45	622.5	51.7	285	12	US-10-140-807-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-09-911-777-2
; Sequence 2, Application US/09911777
; Patent No. US20020037852A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: APOTEC S.A.
; APPLICANT: BROWNING, Jeffrey
; APPLICANT: AMBROSE, Christine
; APPLICANT: MACKAY, Fabienne
; APPLICANT: TSCHOPP, Jurg
; APPLICANT: SCHNEIDER, Pascal
; TITLE OF INVENTION: in the Modulation of B-Cell Response
; FILE REFERENCE: A070 US
; CURRENT APPLICATION NUMBER: US/09/911,777
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/117,169
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 60/143,228
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: PCT/US00/01788
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 232
; TYPE: PPT
; ORGANISM: Murine

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Best Local Similarity 100.0%; Pred. No. 6.4e-120;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 MNLRLMELQSYRGSATPAAAKLLTPAAPRPHNSRGRHNRRAFFPGPEETEODVLSAPPAL 120
QY 121 RNIIODCLQIADSDTPTRKGTTFVFWLLSFKGNALYSQVLYTDFIFAMGHVQRKK 180
DB 121 RNIIODCLQIADSDTPTRKGTTFVFWLLSFKGNALYSQVLYTDFIFAMGHVQRKK 180
QY 181 VHVFGDELSVTLFRCIQLNLEBDEIQLAIPRENAQISRNGDDTFFGALKLL 232
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RESULT 2
US-10-045-574A-2
; Sequence 2, Application US/10045574A
; Publication No. US20030095967A1
; GENERAL INFORMATION:
; APPLICANT: MACKAY, Fabienne
; APPLICANT: KALLEED, Susan
; TITLE OF INVENTION: BUFF, Inhibitors Thereof and Their Use
; TITLE OF INVENTION: In the Modulation of B-Cell Response and Treatment of
; FILE REFERENCE: 08201.0024-01000
; CURRENT APPLICATION NUMBER: US/10/045,574A
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/117,169
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 60/143,228
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: PCT/US00/01788
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/911,777
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 22
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; SEQ ID NO 2
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Murine
US-10-045-574A-2

Query Match 100.0%; Score 1204; DB 15; Length 232;
Best Local Similarity 100.0%; Pred. No. 6.4e-120; Indels 0; Gaps 0;
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DB 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGAVLLSSFTAMSLYQLAALQADL 60
QY 61 MNLRLMELQSYRGSATPAAAKLLTPAAPRPHNSRGRHNRRAFFPGPEETEODVLSAPPAL 120
DB 61 MNLRLMELQSYRGSATPAAAKLLTPAAPRPHNSRGRHNRRAFFPGPEETEODVLSAPPAL 120
QY 121 RNIIODCLQIADSDTPTRKGTTFVFWLLSFKGNALYSQVLYTDFIFAMGHVQRKK 180
DB 121 RNIIODCLQIADSDTPTRKGTTFVFWLLSFKGNALYSQVLYTDFIFAMGHVQRKK 180
QY 181 VHVFGDELSVTLFRCIQLNLEBDEIQLAIPRENAQISRNGDDTFFGALKLL 232
DB 181 VHVFGDELSVTLFRCIQLNLEBDEIQLAIPRENAQISRNGDDTFFGALKLL 232

RESULT 3
US-09-929-493-39
; Sequence 39, Application US/09929493
; Patent No. US20020115112A1
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Neutrokine-alpha and Neutrokine-alpha Splice Variant
; FILE REFERENCE: PF343P4
; CURRENT APPLICATION NUMBER: US/09/929,493

; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/225,628
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/227,008
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/234,338
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/240,806
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/250,020
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/296,122
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/304,809
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-929-493-39

Query Match 91.7%; Score 1103.5; DB 10; Length 309;
Best Local Similarity 74.4%; Pred. No. 4.9e-109; Indels 77; Gaps 5;
Matches 230; Conservative 0; Mismatches 2;
QY 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGA-----VLLSS 43
DB 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGANFICDRGLLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLMLRLMELQSYRGSATPAAA-----KULTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLMLRLMELQSYRGSATPAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRRAFFPGPEETEODVLSAPPA-----LRNIIDQCILQIADSDTP 137
DB 121 GHRNRRAFFPGPEETEODVLSAPPA-----LRNIIDQCILQIADSDTP 180
QY 138 TIRKGTTFVFWLLSFKRGNAL-----YSQVLYTDFIFAMGHVQRKK 180
DB 181 TIRKGTTFVFWLLSFKRGNALKEENKIVVRGTGYFFIYSQVLYTDFIFAMGHVQRKK 240
QY 181 VHVFGDELSVTLFRCIQLN-----LEEGDEIQLAIPRENAQISRNGDD 223
DB 241 VHVFGDELSVTLFRCIQLNMPKTLPPNNSCYSAGIARLEEGDEIQLAIPRENAQISRNGDD 300
QY 224 TFFGALKLL 232
DB 301 TFFGALKLL 309

RESULT 4
US-09-779-050A-4
; Sequence 4, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 309

QY TYPE: PRT
ORGANISM: Mus musculus
US-09-779-050A-4

Query Match 91.7%; Score 1103.5; DB 10; Length 309;
Best Local Similarity 74.4%; Pred. No. 4.9e-109;
Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;
QY 1 MDESATLPPPCLCFCSEKEDMKVGYDPIIPQKEGA-----VLLSS 43
DB 1 MDESATLPPPCLCFCSEKEDMKVGYDPIIPQKEGAWFGICRDGRLLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLITPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRRAPPGPEETEEDVDLSAPPA-----LRNIODCLQIADSDTP 137
DB 121 GHRNRRAPPGPEETEEDVDLSAPPAPCLPGCRHSQHDNDGNNLRNIIODCLQIADSDTP 180
QY 138 TIRKGTTFVFWLLSFKRGNAL-----YSOVLYTDFIFAMGHVIOQRK 180
DB 181 TIRKGTTFVFWLLSFKRGNALEEKENKIVVROTGYFFIYSOVLYTDFIFAMGHVIOQRK 240
QY 181 VHVFGDELSLVTLFRCIQN-----LEEDEIQALAI PRENAQISRNGDD 223
DB 241 VHVFGDELSLVTLFRCIQNMPKTLPNNSCYLAGIARLEEGDEIQALAI PRENAQISRNGDD 300
QY 224 TFFGALKLL 232
DB 301 TFFGALKLL 309

RESULT 5

US-09-880-748-3230
Sequence 3230, Application US/09880748
Publication No. US2003005937A1

GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys

FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3230
LENGTH: 309
TYPE: PRT
ORGANISM: Mus musculus
US-09-880-748-3230

Query Match 91.7%; Score 1103.5; DB 11; Length 309;
Best Local Similarity 74.4%; Pred. No. 4.9e-109;
Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;
QY 1 MDESATLPPPCLCFCSEKEDMKVGYDPIIPQKEGA-----VLLSS 43
DB 1 MDESATLPPPCLCFCSEKEDMKVGYDPIIPQKEGAWFGICRDGRLLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLITPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120

QY 95 GHRNRRAPPGPEETEEDVDLSAPPA-----LRNIODCLQIADSDTP 137
DB 121 GHRNRRAPPGPEETEEDVDLSAPPAPCLPGCRHSQHDNDGNNLRNIIODCLQIADSDTP 180
QY 138 TIRKGTTFVFWLLSFKRGNAL-----YSOVLYTDFIFAMGHVIOQRK 180
DB 181 TIRKGTTFVFWLLSFKRGNALEEKENKIVVROTGYFFIYSOVLYTDFIFAMGHVIOQRK 240
QY 181 VHVFGDELSLVTLFRCIQN-----LEEDEIQALAI PRENAQISRNGDD 223
DB 241 VHVFGDELSLVTLFRCIQNMPKTLPNNSCYLAGIARLEEGDEIQALAI PRENAQISRNGDD 300
QY 224 TFFGALKLL 232
DB 301 TFFGALKLL 309

RESULT 6

US-09-932-613-175
Sequence 175, Application US/09932613
Publication No. US20030091565A1

GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patent In version 3.1
SEQ ID NO 175
LENGTH: 309
TYPE: PRT
ORGANISM: mouse
US-09-932-613-175

Query Match 91.7%; Score 1103.5; DB 11; Length 309;
Best Local Similarity 74.4%; Pred. No. 4.9e-109;
Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;

QY 1 MDESATLPPPCLCFCSEKEDMKVGYDPIIPQKEGA-----VLLSS 43
DB 1 MDESATLPPPCLCFCSEKEDMKVGYDPIIPQKEGAWFGICRDGRLLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLITPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRRAPPGPEETEEDVDLSAPPA-----LRNIODCLQIADSDTP 137
DB 121 GHRNRRAPPGPEETEEDVDLSAPPAPCLPGCRHSQHDNDGNNLRNIIODCLQIADSDTP 180
QY 138 TIRKGTTFVFWLLSFKRGNAL-----YSOVLYTDFIFAMGHVIOQRK 180
DB 181 TIRKGTTFVFWLLSFKRGNALEEKENKIVVROTGYFFIYSOVLYTDFIFAMGHVIOQRK 240
QY 181 VHVFGDELSLVTLFRCIQN-----LEEDEIQALAI PRENAQISRNGDD 223
DB 241 VHVFGDELSLVTLFRCIQNMPKTLPNNSCYLAGIARLEEGDEIQALAI PRENAQISRNGDD 300
QY 224 TFFGALKLL 232
DB 301 TFFGALKLL 309

RESULT 7

US-10-270-487-39
Sequence 39, Application US/10270487
Publication No. US20030175208A1

GENERAL INFORMATION:

138	QY	TIRGTTGTFVPWLLSFKRGNAL	-----YSOVLVTDPIFAMGHVIQRKK	181
181	Db	TIRGTTGTFVPWLLSFKRGNALEEKNI	VVRGTGYPIYSQVLVTDPIFAMGHVIQRKK	240
181	QY	VHVGDELSLVTLPFRCIQN	-----LEEGDSIQIAIPRENAQISRNGDD	223
241	Db	VHVGDELSLVTLPFRCIQNMPKTL	PNNNSCVSAGIARLEEGDSIQIAIPRENAQISRNGDD	300

; PRIOR FILING DATE: 2000-08-15
 ; PRIOR APPLICATION NUMBER: 60/227,008
 ; PRIOR FILING DATE: 2000-08-23
 ; PRIOR APPLICATION NUMBER: 60/234,338
 ; PRIOR FILING DATE: 2000-09-22

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: PRIOR FILING DATE: 2001-03-06
: PRIOR APPLICATION NUMBER: 60/293,499
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/296,122
: PRIOR FILING DATE: 2001-06-07
: PRIOR APPLICATION NUMBER: 60/304,809
: PRIOR FILING DATE: 2001-07-13
: NUMBER OF SEQ ID NOS: 47
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 40
: LENGTH: 290

```

TYPE: PRT
ORGANISM: Mus Musculus
US-09-929-493-40

Query Match 83.0%; Score 999; DB 10; Length 290;
Best Local Similarity 71.9%; Pred. No. 6.2e-98;
Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESATLPPPCLCFCSEKGDVDSAPPALRNIIQDCLQIADSDPTTIRKGTTFVFWLLSFK 43
DB 1 MDESATLPPPCLCFCSEKGDVDSAPPALRNIIQDCLQIADSDPTTIRKGTTFVFWLLSFK 60
QY 44 SFTMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLTTPAAPRPHNSR 94
DB 61 SFTMSLYQLAALQADLNLRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRAPPGPEETEODVLSAPPALRNIIQDCLQIADSDPTTIRKGTTFVFWLLSFK 154
DB 121 GHRNRAPPGPEETEODVLSAPPALRNIIQDCLQIADSDPTTIRKGTTFVFWLLSFK 178
QY 155 RGNAL-----YSQVLYTDFIFAMGHVIOQRKKVHVFGDELSLTLFRCI 197
DB 179 RGNALKEENKIVVRQTGYFFIYSQVLYTDFIFAMGHVIOQRKKVHVFGDELSLTLFRCI 238
QY 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 232
DB 239 QNMPKTLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 290

RESULT 10
US-09-880-748-3231
Sequence 3231, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3231
LENGTH: 290
TYPE: PRT
ORGANISM: Mus musculus
US-09-880-748-3231

Query Match 83.0%; Score 999; DB 11; Length 290;
Best Local Similarity 71.9%; Pred. No. 6.2e-98;
Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESATLPPPCLCFCSEKGDVDSAPPALRNIIQDCLQIADSDPTTIRKGTTFVFWLLSFK 43
DB 1 MDESATLPPPCLCFCSEKGDVDSAPPALRNIIQDCLQIADSDPTTIRKGTTFVFWLLSFK 60
QY 44 SFTMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLTTPAAPRPHNSR 94
DB 61 SFTMSLYQLAALQADLNLRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRAPPGPEETEODVLSAPPALRNIIQDCLQIADSDPTTIRKGTTFVFWLLSFK 154
DB 121 GHRNRAPPGPEETEODVLSAPPALRNIIQDCLQIADSDPTTIRKGTTFVFWLLSFK 178

QY 155 RGNAL-----YSQVLYTDFIFAMGHVIOQRKKVHVFGDELSLTLFRCI 197
DB 179 RGNALKEENKIVVRQTGYFFIYSQVLYTDFIFAMGHVIOQRKKVHVFGDELSLTLFRCI 238
QY 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 232
DB 239 QNMPKTLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 290

RESULT 11
US-09-932-613-176
Sequence 176, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT: DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patent In version 3.1
SEQ ID NO 176
LENGTH: 290
TYPE: PRT
ORGANISM: mouse
US-09-932-613-176

Query Match 83.0%; Score 999; DB 11; Length 290;
Best Local Similarity 71.9%; Pred. No. 6.2e-98;
Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESATLPPPCLCFCSEKGDVDSAPPALRNIIQDCLQIADSDPTTIRKGTTFVFWLLSFK 43
DB 1 MDESATLPPPCLCFCSEKGDVDSAPPALRNIIQDCLQIADSDPTTIRKGTTFVFWLLSFK 60
QY 44 SFTMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLTTPAAPRPHNSR 94
DB 61 SFTMSLYQLAALQADLNLRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRAPPGPEETEODVLSAPPALRNIIQDCLQIADSDPTTIRKGTTFVFWLLSFK 154
DB 121 GHRNRAPPGPEETEODVLSAPPALRNIIQDCLQIADSDPTTIRKGTTFVFWLLSFK 178
QY 155 RGNAL-----YSQVLYTDFIFAMGHVIOQRKKVHVFGDELSLTLFRCI 197
DB 179 RGNALKEENKIVVRQTGYFFIYSQVLYTDFIFAMGHVIOQRKKVHVFGDELSLTLFRCI 238
QY 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 232
DB 239 QNMPKTLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 290

RESULT 12
US-10-270-487-40
Sequence 40, Application US/10270487
Publication No. US20030175208A1
GENERAL INFORMATION:
APPLICANT: Yu et al.
TITLE OF INVENTION: Neutrokine-alpha and Neutrokine-alpha Splice Variant
FILE REFERENCE: PF343P5
CURRENT APPLICATION NUMBER: US/10/270,487
CURRENT FILING DATE: 2002-10-16
PRIOR FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/368,548
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/336,726
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/331,478
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/330,835

PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 60/329,747
PRIOR FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 60/329,508
PRIOR FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/929,493
PRIOR FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 60/225,628
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/227,008
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 60/234,338
PRIOR FILING DATE: 2000-09-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 40
LENGTH: 290
TYPE: PRT
ORGANISM: Mus musculus
US-10-270-487-40

Query Match 83.0%; Score 999; DB 12; Length 290;
Best Local Similarity 71.9%; Pred. No. 6.2e-98;
Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;
QY 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGA-----VLLSS 43
DB 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGAWFICRDRGRLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLMNLRMELOSRYGSGATPAAA-----KLTTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLMNLRMELOSRYGSGATPAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRAPPGPEETEQQVDLSAPPALRNIIQDCLQIADSDTPTIRKGTTFVFPWLLSFK 154
DB 121 GHRNRAPPGPEETEQQVDLSAPPA--PCLPGCRHSQHDGMLNRNRTYTFVFPWLLSFK 178
QY 155 RGNAL-----YSQVLYTDFIFAMGHVIQKRVHVFGEDELSTLTLFRCI 197
DB 179 RGNALKEENKIVVRQTGYFFIYSQVLYTDFIFAMGHVIQKRVHVFGEDELSTLTLFRCI 238
QY 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 232
DB 239 QNMPKTLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 290
US-10-270-487-40

RESULT 13
US-09-932-322-176
Sequence 176, Application US/09932322
Publication No. US20030194743A1
GENERAL INFORMATION:
APPLICANT: Dyax Corp.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Ladner, Robert Charles
TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLyS)
FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US
CURRENT APPLICATION NUMBER: US/09/932,322
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 176
LENGTH: 290
TYPE: PRT
ORGANISM: mouse
US-09-932-322-176

Query Match 83.0%; Score 999; DB 12; Length 290;
Best Local Similarity 71.9%; Pred. No. 6.2e-98;
Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGA-----VLLSS 43
DB 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGAWFICRDRGRLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLMNLRMELOSRYGSGATPAAA-----KLTTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLMNLRMELOSRYGSGATPAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRAPPGPEETEQQVDLSAPPALRNIIQDCLQIADSDTPTIRKGTTFVFPWLLSFK 154
DB 121 GHRNRAPPGPEETEQQVDLSAPPA--PCLPGCRHSQHDGMLNRNRTYTFVFPWLLSFK 178
QY 155 RGNAL-----YSQVLYTDFIFAMGHVIQKRVHVFGEDELSTLTLFRCI 197
DB 179 RGNALKEENKIVVRQTGYFFIYSQVLYTDFIFAMGHVIQKRVHVFGEDELSTLTLFRCI 238
QY 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 232
DB 239 QNMPKTLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 290
US-10-214-065-8
Sequence 8, Application US/10214065
Publication No. US20030023038A1
GENERAL INFORMATION:
APPLICANT: Biogen, Inc.
APPLICANT: Remnet, Paul D.
APPLICANT: Thompson, Jeffrey S.
APPLICANT: Ambrose, Christine
APPLICANT: Cachero, Teresa G.
TITLE OF INVENTION: Heterologous Polypeptide of the TNF
FILE REFERENCE: A092 US
CURRENT APPLICATION NUMBER: US/10/214,065
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: 60/181,670
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: PCT/US01/04121
PRIOR FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 290
TYPE: PRT
ORGANISM: Homo sapien
US-10-214-065-8

Query Match 83.0%; Score 999; DB 15; Length 290;
Best Local Similarity 71.9%; Pred. No. 6.2e-98;
Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;
QY 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGA-----VLLSS 43
DB 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGAWFICRDRGRLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLMNLRMELOSRYGSGATPAAA-----KLTTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLMNLRMELOSRYGSGATPAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRAPPGPEETEQQVDLSAPPALRNIIQDCLQIADSDTPTIRKGTTFVFPWLLSFK 154
DB 121 GHRNRAPPGPEETEQQVDLSAPPA--PCLPGCRHSQHDGMLNRNRTYTFVFPWLLSFK 178
QY 155 RGNAL-----YSQVLYTDFIFAMGHVIQKRVHVFGEDELSTLTLFRCI 197
DB 179 RGNALKEENKIVVRQTGYFFIYSQVLYTDFIFAMGHVIQKRVHVFGEDELSTLTLFRCI 238
QY 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 232
DB 239 QNMPKTLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 290
US-10-214-065-8

RESULT 15

US-09-929-493-38
; Sequence 38, Application US/09929493
; Patent No. US20020115112A1
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Neutrokin-alpha and Neutrokin-alpha Splice Variant
; FILE REFERENCE: PF343P4
; CURRENT APPLICATION NUMBER: US/09/929,493
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/225,628
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/227,008
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/234,338
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/240,806
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/250,020
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/296,122
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/304,809
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 38
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-929-493-38

Query Match 82.4%; Score 992.5; DB 10; Length 289;
Best Local Similarity 70.1%; Pred. No. 3.1e-97;
Matches 211; Conservative 3; Mismatches 6; Indels 81; Gaps 6;

QY 1 MDESAKTLPPCLCFCEKGEKMGVGYDITPOKEGA-----VLLSS 43
DB 1 MDESAKTLPPCLCFCEKGEKMGVGYDITPOKEGAWFGICRDLAATLLALLSS 60

QY 44 SFTAMSLYQLAALQADLMRLMELQSYRGSAAPAAA-----KLTTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLMRLMELQSYRGSAAPAAAPELTAGVKLLTPAAPRPHNSR 120

QY 95 GHRNRAFPPEPTEQDVLDSAPPA-----LRNIIQDCLQLIADSDTP 137
DB 121 GHRNRAFPPEPTEQDVLDSAPPAFLPCGRHSQHDDNGMNLNIIQDCLQLIADSDTP 180

QY 138 -----TIRKGTTFVFWLLSFKRGNALYSQVLYTDPFAMGHVIOKKVHVPGEDEL 188
DB 181 ALEEKENKIWRQTGYFFI-----YSQVLYTDPFAMGHVIOKKVHVPGEDEL 228

QY 189 SLVTLFRCLQN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKL 231
DB 229 SLVTLFRCLQNPKLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKL 288

QY 232 L 232
DB 289 L 289

Search completed: February 3, 2004, 08:02:17
Job time : 225.782 secs

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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:43:37 ; Search time 14.9511 Seconds
(without alignments)
656.548 Million cell updates/sec

Title: US-09-911-777-2

Perfect score: 1204

Sequence: 1 MDESATLPPCLCFCEKSG.....ENAIQRNGDDTFFGALKL.232

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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/prodata/1/iaa/FCUS_COMB.pep:*

6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match Length	ID	Description
1	992.5	82.4	289	4	US-09-589-287B-38
2	992.5	82.4	289	4	US-09-588-947A-38
3	622.5	51.7	285	3	US-09-286-529-1
4	622.5	51.7	285	4	US-09-589-287B-2
5	622.5	51.7	285	4	US-09-496-118B-1
6	622.5	51.7	285	4	US-09-565-423-2
7	622.5	51.7	285	4	US-09-879-919-23
8	622.5	51.7	285	4	US-09-588-947A-2
9	582.5	48.4	219	4	US-09-589-287B-30
10	582.5	48.4	219	4	US-09-588-947A-30
11	578.5	48.0	219	4	US-09-589-287B-28
12	578.5	48.0	219	4	US-09-588-947A-28
13	531	44.1	266	4	US-09-589-287B-19
14	531	44.1	266	4	US-09-879-919-24
15	531	44.1	266	4	US-09-588-947A-19
16	526	43.7	174	4	US-09-496-118B-5
17	464	38.5	155	4	US-09-589-287B-23
18	464	38.5	155	4	US-09-588-947A-23
19	463	38.5	145	3	US-09-286-529-21
20	149	12.4	250	3	US-08-883-086-2
21	149	12.4	250	4	US-09-565-423-3
22	148	12.3	205	3	US-09-286-529-5
23	147	12.2	234	4	US-09-157-864-2
24	141	11.7	233	4	US-10-082-260-2
25	141	11.7	233	4	US-08-815-783-2
26	141	11.7	233	4	US-09-879-919-2
27	141	11.7	247	4	US-09-157-864-4

28	141	11.7	250	3	US-09-153-927-4	Sequence 4, Appli
29	141	11.7	250	4	US-09-879-919-11	Sequence 11, Appl
30	139	11.5	234	4	US-09-879-919-13	Sequence 13, Appl
31	125	10.4	136	4	US-09-589-287B-20	Sequence 20, Appl
32	125	10.4	136	4	US-09-588-947A-20	Sequence 20, Appl
33	125	10.4	147	3	US-08-883-086-3	Sequence 3, Appli
34	125	10.4	168	4	US-10-082-260-4	Sequence 4, Appli
35	125	10.4	168	4	US-08-815-783-4	Sequence 4, Appli
36	125	10.4	168	4	US-09-879-919-4	Sequence 4, Appli
37	91	7.6	539	2	US-08-735-041A-2	Sequence 2, Appli
38	91	7.6	539	3	US-09-190-476B-2	Sequence 2, Appli
39	91	7.6	539	3	US-09-190-889A-2	Sequence 2, Appli
40	91	7.6	539	3	US-09-190-938B-2	Sequence 2, Appli
41	91	7.6	539	5	PCT-US95-09261-2	Sequence 2, Appli
42	81	6.7	452	4	US-09-252-991A-18948	Sequence 18948, A
43	78.5	6.5	15281	2	US-08-471-119A-2	Sequence 2, Appli
44	77.5	6.4	454	3	US-08-348-518C-4	Sequence 4, Appli
45	77.5	6.4	454	3	US-08-476-509B-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-589-287B-38

; Sequence 38, Application US/09589287B

; Patent No. 6403770

; GENERAL INFORMATION:

; APPLICANT: Yu et al.

; TITLE OF INVENTION: Antibodies to Neutrokin-alpha

; FILE REFERENCE: PF343P3C1

; CURRENT APPLICATION NUMBER: US/09/589,287B

; CURRENT FILING DATE: 2000-06-08

; Prior application data removed - check PALM or file wrapper

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 38

; LENGTH: 289

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-589-287B-38

Query Match 82.4%; Score 992.5; DB 4; Length 289;
Best Local Similarity 70.1%; Pred. No. 4.1e-107;
Matches 211; Conservative 3; Mismatches 6; Indels 81; Gaps 6;

Qy	1	MDESATLPPCLCFCEKSGEDMKVGYDPITPQKEGA-----VLLSS	43
Db	1	MDESATLPPCLCFCEKSGEDMKVGYDPITPQKEGAWFGICRDGRLLAATLLALLSS	60
Qy	44	SFTAMSLYQLAALQADLANLRLMELQSYRGSATPAAA-----KLTPAAPRPHNSR	94
Db	61	SFTAMSLYQLAALQADLANLRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR	120
Qy	95	GHRNRRAPFGPEETEQDVLDSAPPA-----LRNIIDCLQLIADSDTP	137
Db	121	GHRNRRAPFGPEETEQDVLDSAPPA-----LRNIIDCLQLIADSDTP	180
Qy	138	-----TTKRGYTFVFWLLSPFRGNALYSQVLYTDPFAMGHVTRKQKVVHFGDEL	188
Db	181	ALEEKENKIVVRQTGYFFI-----YSQVLYTDPFAMGHVTRKQKVVHFGDEL	228
Qy	189	SIATLFRICN-----LEEDEIQLAI PRENAOISRNGDDTFFGALKL	231
Db	229	SIATLFRICNPKTLPNNSCYSAGIARLEEDEIQLAI PRENAOISRNGDDTFFGALKL	288
Qy	232	L 232	
Db	289	L 289	

RESULT 2

US-09-588-947A-38

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; Sequence 38, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C2
; CURRENT APPLICATION NUMBER: US/09/588,947A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/130,696
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 60/131,278
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131,673
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/136,784
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,659
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: 60/145,824
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 60/167,239
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 60/168,624
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: PCT/US96/17957
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 38
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-588-947A-38

; Query Match 82.4%; Score 992.5; DB 4; Length 289;
; Best Local Similarity 70.1%; Pred. No. 4.1e-107;
; Matches 211; Conservative 3; Mismatches 6; Indels 81; Gaps 6;

QY 1 MDESATLPPPCLCFCSEKEDMKVGYDPTTPOKEEGA-----VLLSS 43
Db 1 MDESATLPPPCLCFCSEKEDMKVGYDPTTPOKEEGAFCIGRDLAATLLALLSS 60
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Db 61 SFTAMSLYQLAALQADLNLNRLMELQSYRGSATPAAAGAPELTAGVKLLTTPA 120
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; Sequence 38, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C2
; CURRENT APPLICATION NUMBER: US/09/588,947A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
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; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
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; PRIOR APPLICATION NUMBER: 60/142,659
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: 60/145,824
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 60/167,239
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; PRIOR APPLICATION NUMBER: 60/168,624
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; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: PCT/US96/17957
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 38
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-588-947A-38

; Query Match 51.7%; Score 622.5; DB 3; Length 285;
; Best Local Similarity 48.7%; Pred. No. 4.5e-64;
; Matches 146; Conservative 23; Mismatches 48; Indels 83; Gaps 7;

QY 1 MDESATLPPPCLCFCSEKEDMKV-GYDPTTPOKEGAV-----LSS 43
Db 1 MDDSTER-EQSRLTSCCLKREEMKLCVSLTPRKESPSVRSSKDGKLLAATLLALLSS 59
QY 44 SFTAMSLYQLAALQADLNLNRLMELQSYRGSATPAAA-----KLLTPAA 86
Db 60 CLTVSVFYQVAALQDGLASLAEQLQGHAEKLPAGAGAPKAGLEAPAVTAGLKFEP 119
QY 87 PRPHNSRGHNRRAFPPEETQDVLSDAPPAALNIIQDCLLIADSDTTIRKGYTF 146
Db 120 PEGNSSQNSRKRVAQGPET-----VTQDCLLIADSETPTIQGSYTF 165
QY 147 VPWLLSPKRGNAL-----YSQVLYTDPFAMGHVQIRKKVHVFGEELS 189
Db 166 VPWLLSPKRGSALEEKENKILVKETGYTFYQVLYTDTKYAMGHVQIRKKVHVFGEELS 225
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Db 226 LVTLFRCTQNMPETLPNNNSCYSAGIAKLEEGDEIQLAIPRENAQISLDGDTFFGALKL 285

RESULT 4
US-09-589-287B-2
; Sequence 2, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2

; Sequence 38, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C2
; CURRENT APPLICATION NUMBER: US/09/588,947A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/130,696
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 60/131,278
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131,673
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/136,784
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,659
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: 60/145,824
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 60/167,239
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 60/168,624
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: PCT/US96/17957
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 38
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-588-947A-38

; Query Match 51.7%; Score 622.5; DB 3; Length 285;
; Best Local Similarity 48.7%; Pred. No. 4.5e-64;
; Matches 146; Conservative 23; Mismatches 48; Indels 83; Gaps 7;

QY 1 MDESATLPPPCLCFCSEKEDMKV-GYDPTTPOKEGAV-----LSS 43
Db 1 MDDSTER-EQSRLTSCCLKREEMKLCVSLTPRKESPSVRSSKDGKLLAATLLALLSS 59
QY 44 SFTAMSLYQLAALQADLNLNRLMELQSYRGSATPAAA-----KLLTPAA 86
Db 60 CLTVSVFYQVAALQDGLASLAEQLQGHAEKLPAGAGAPKAGLEAPAVTAGLKFEP 119
QY 87 PRPHNSRGHNRRAFPPEETQDVLSDAPPAALNIIQDCLLIADSDTTIRKGYTF 146
Db 120 PEGNSSQNSRKRVAQGPET-----VTQDCLLIADSETPTIQGSYTF 165
QY 147 VPWLLSPKRGNAL-----YSQVLYTDPFAMGHVQIRKKVHVFGEELS 189
Db 166 VPWLLSPKRGSALEEKENKILVKETGYTFYQVLYTDTKYAMGHVQIRKKVHVFGEELS 225
QY 190 LVTLFRCTQN-----LEEGDEIQLAIPRENAQISRNGDDTFFGALKL 232
Db 226 LVTLFRCTQNMPETLPNNNSCYSAGIAKLEEGDEIQLAIPRENAQISLDGDTFFGALKL 285

RESULT 3
US-09-286-529-1
; Sequence 1, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-286-529-1

; Sequence 38, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C2
; CURRENT APPLICATION NUMBER: US/09/588,947A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/130,696
; PRIOR FILING DATE: 1999-04-23
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; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131,673
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/136,784
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,659
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: 60/145,824
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 60/167,239
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 60/168,624
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: PCT/US96/17957
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 38
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-588-947A-38

; Query Match 82.4%; Score 992.5; DB 4; Length 289;
; Best Local Similarity 70.1%; Pred. No. 4.1e-107;
; Matches 211; Conservative 3; Mismatches 6; Indels 81; Gaps 6;

QY 1 MDESATLPPPCLCFCSEKEDMKVGYDPTTPOKEEGA-----VLLSS 43
Db 1 MDESATLPPPCLCFCSEKEDMKVGYDPTTPOKEEGAFCIGRDLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLNLNRLMELQSYRGSATPAAA-----KLLTPAA 94
Db 61 SFTAMSLYQLAALQADLNLNRLMELQSYRGSATPAAAGAPELTAGVKLLTTPA 120
QY 95 GHRNRRAFPPEETQDVLSDAPPA-----LRNIIQDCLLIADSDTP 137
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; LENGTH: 285

; TYPE: PRT

; ORGANISM: human

US-09-589-287B-2

Query Match 51.7%; Score 622.5; DB 4; Length 285;

Best Local Similarity 48.7%; Pred. No. 4.5e-64;

Matches 146; Conservative 23; Mismatches 48; Indels 83; Gaps 7;

QY 1 MDESAKTLPPPCLCFCSEKGEKDMKV-GYDPTTPQKEGAV-----LLSS 43
DB 1 MDDSTER-EQSRLTSCCLKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLLSC 59
QY 44 SFTAMSLYQLAALQADLMNLMELQSYRGSATPAAA-----KLLTPAA 86
DB 60 CLTVVSFYQVAALQDGLASRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEP 119
QY 87 PRPHNSSRGRNRRAPPGPEETEQQVDLSAPPALNIIQDCLLIADSDTPTIRKGTTF 146
DB 120 PEGNSSQNSRNKRAVQGPET-----VTQDCLLIADSETPTIQKSYTF 165
QY 147 VPMLLSFKRGNAL-----YSQVLYTDPFAMGHVIOKKVHVFGDELS 189
DB 166 VPMLLSFKRGSALEBKENKILVKETGYFFIYGVLYTDKTYAMGHVIOKKVHVFGDELS 225
QY 190 LVTLFRCIQN-----LEEDEIQLAIPRENAQISRNGDDTFFGALKIL 232
DB 226 LVTLFRCIQNMPETLPNNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDDVTFFGALKIL 285

RESULT 5

US-09-496-118B-1

Sequence 1, Application US/09496118B

Patent No. 6475986

GENERAL INFORMATION:

APPLICANT: Aggarwal, Bharat B.

TITLE OF INVENTION: Uses of THANK, a TNF homologue that Activates

FILE OF INVENTION: Apoptosis

FILE REFERENCE: D6206

CURRENT APPLICATION NUMBER: US/09/496,118B

CURRENT FILING DATE: 2000-02-01

PRIOR APPLICATION NUMBER: US 60/118,531

PRIOR FILING DATE: 1999-02-02

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 1

LENGTH: 285

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: amino acid sequence of THANK protein

US-09-496-118B-1

Query Match

51.7%; Score 622.5; DB 4; Length 285;

Best Local Similarity 48.7%; Pred. No. 4.5e-64;

Matches 146; Conservative 23; Mismatches 48; Indels 83; Gaps 7;

QY 1 MDESAKTLPPPCLCFCSEKGEKDMKV-GYDPTTPQKEGAV-----LLSS 43
DB 1 MDDSTER-EQSRLTSCCLKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLLSC 59
QY 44 SFTAMSLYQLAALQADLMNLMELQSYRGSATPAAA-----KLLTPAA 86
DB 60 CLTVVSFYQVAALQDGLASRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEP 119
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DB 120 PEGNSSQNSRNKRAVQGPET-----VTQDCLLIADSETPTIQKSYTF 165
QY 147 VPMLLSFKRGNAL-----YSQVLYTDPFAMGHVIOKKVHVFGDELS 189
DB 166 VPMLLSFKRGSALEBKENKILVKETGYFFIYGVLYTDKTYAMGHVIOKKVHVFGDELS 225
QY 190 LVTLFRCIQN-----LEEDEIQLAIPRENAQISRNGDDTFFGALKIL 232

DB 226 LVTLFRCIQNMPETLPNNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDDVTFFGALKIL 285

RESULT 6

US-09-565-423-2

Sequence 2, Application US/09565423

Patent No. 6475987

GENERAL INFORMATION:

APPLICANT: Shu, Hong-Bing

TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

FILE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 2879-72

CURRENT APPLICATION NUMBER: US/09/565,423

CURRENT FILING DATE: 2000-05-05

PRIOR APPLICATION NUMBER: UNKNOWN

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 60/132,892

PRIOR FILING DATE: 1999-05-06

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 285

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: primer

US-09-565-423-2

Query Match

51.7%; Score 622.5; DB 4; Length 285;

Best Local Similarity 48.7%; Pred. No. 4.5e-64;

Matches 146; Conservative 23; Mismatches 48; Indels 83; Gaps 7;

QY 1 MDESAKTLPPPCLCFCSEKGEKDMKV-GYDPTTPQKEGAV-----LLSS 43
DB 1 MDDSTER-EQSRLTSCCLKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLLSC 59
QY 44 SFTAMSLYQLAALQADLMNLMELQSYRGSATPAAA-----KLLTPAA 86
DB 60 CLTVVSFYQVAALQDGLASRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEP 119
QY 87 PRPHNSSRGRNRRAPPGPEETEQQVDLSAPPALNIIQDCLLIADSDTPTIRKGTTF 146
DB 120 PEGNSSQNSRNKRAVQGPET-----VTQDCLLIADSETPTIQKSYTF 165
QY 147 VPMLLSFKRGNAL-----YSQVLYTDPFAMGHVIOKKVHVFGDELS 189
DB 166 VPMLLSFKRGSALEBKENKILVKETGYFFIYGVLYTDKTYAMGHVIOKKVHVFGDELS 225
QY 190 LVTLFRCIQN-----LEEDEIQLAIPRENAQISRNGDDTFFGALKIL 232
DB 226 LVTLFRCIQNMPETLPNNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDDVTFFGALKIL 285

RESULT 7

US-09-879-919-23

Sequence 23, Application US/09879919

Patent No. 6541224

GENERAL INFORMATION:

APPLICANT: Yu, Guo-Liang, et al.

TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon

FILE REFERENCE: PF253P1

CURRENT APPLICATION NUMBER: US/09/879,919

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,978

PRIOR FILING DATE: 2001-03-23

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/254,875

PRIOR FILING DATE: 2000-12-13

PRIOR APPLICATION NUMBER: 60/241,952

; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-23

Query Match 51.7%; Score 622.5; DB 4; Length 285;
Best Local Similarity 48.7%; Pred. No. 4.5e-64;
Matches 146; Conservative 23; Mismatches 48; Indels 83; Gaps 7;
Qy 1 MDESAKTLPPCLCFCEKGEKMKV-GYDPTTPOKEGAV-----LLSS 43
Db 1 MDDSTER-EQSLRTSLCKRREMKLKCVCVILPRKESPSVRSSKDGKLLAATLLALLLSC 59
Qy 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLLTPAA 86
Db 60 CLTVVSFYQVAALQDGLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEP 119
Qy 87 PRPHNSRGHNRRAFPPEETEODVLSAPPALNIIQDCLQIADSDTPTIRKGTYTF 146
Db 120 PEGNSSQNSRNRKRAVQGPET-----VTQDCIQLIADSETPTIQKSYTF 165
Qy 147 VPWLLSFRKGNAL-----YSQVLYTDPFAMGHVIOKKVHVFGDELS 189
Db 166 VPWLLSFRKGSALBEKENKILVKETGYFFYQGVLYTDKTYAMGHLIQKKVHVFGDELS 225
Qy 190 LVTFLFRICQN-----LEEDEIQLAIPRENAQISRNGDDTFFGALKLL 232
Db 226 LVTFLFRICQNMPETLPNNNSCYSAGIAKLEEGDELQALIPRENAQISLDGDTFFGALKLL 285

RESULT 8

US-09-588-947A-2
; Sequence 2, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; CURRENT APPLICATION NUMBER: US/09/588,947A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/130,696
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 60/131,278
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131,673
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/136,784
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,659

; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: 60/145,824
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 60/167,239
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 60/168,624
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: PCT/US96/17957
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-588-947A-2

Query Match 51.7%; Score 622.5; DB 4; Length 285;
Best Local Similarity 48.7%; Pred. No. 4.5e-64;
Matches 146; Conservative 23; Mismatches 48; Indels 83; Gaps 7;
Qy 1 MDESAKTLPPCLCFCEKGEKMKV-GYDPTTPOKEGAV-----LLSS 43
Db 1 MDDSTER-EQSLRTSLCKRREMKLKCVCVILPRKESPSVRSSKDGKLLAATLLALLLSC 59
Qy 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLLTPAA 86
Db 60 CLTVVSFYQVAALQDGLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEP 119
Qy 87 PRPHNSRGHNRRAFPPEETEODVLSAPPALNIIQDCLQIADSDTPTIRKGTYTF 146
Db 120 PEGNSSQNSRNRKRAVQGPET-----VTQDCIQLIADSETPTIQKSYTF 165
Qy 147 VPWLLSFRKGNAL-----YSQVLYTDPFAMGHVIOKKVHVFGDELS 189
Db 166 VPWLLSFRKGSALBEKENKILVKETGYFFYQGVLYTDKTYAMGHLIQKKVHVFGDELS 225
Qy 190 LVTFLFRICQN-----LEEDEIQLAIPRENAQISRNGDDTFFGALKLL 232
Db 226 LVTFLFRICQNMPETLPNNNSCYSAGIAKLEEGDELQALIPRENAQISLDGDTFFGALKLL 285

RESULT 9

US-09-589-287B-30
; Sequence 30, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-30

Query Match 48.4%; Score 582.5; DB 4; Length 219;
Best Local Similarity 54.5%; Pred. No. 1.4e-59;
Matches 127; Conservative 16; Mismatches 25; Indels 65; Gaps 4;
QY 51 YQLAALQADLMNRMELQSYRGSATPAAA-----KLLTPAAPRPHNSS 93
Db 1 YQVAAVQGDLSRAELQSHAEKLPARAPAKAGLGEAPAVTAGLKIFEPPAPGEGNSS 60
QY 94 RGHNRRAFPGPETEEDVDLSAPPALRNIIODCLQLIADSDTPTRKGTTFVFWLLSF 153
Db 61 QSSRNKRAIOGAET-----VIQDCIQLIADSETPTIQKSYTFVFWLLSF 106
QY 154 KRGNAL-----YSQVLYTDPFAMGHVIOKKVHVFGDELSTVTLFRC 196
Db 107 KRGSALKEENKILVKETGYFFIYQVLYTDTKYAMGHLIQKKVHVFGDELSTVTLFRC 166
QY 197 IQN-----LEEGBEIOQLAIAPRENAQISRGDDTFFGALKLL 232
Db 167 IQNMPETLPNNSCYSAGIAKLEEGDELQALAIAPRENAQISLDGDTFFGALKLL 219

RESULT 10
US-09-588-947A-30
; Sequence 30, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C2
; CURRENT APPLICATION NUMBER: US/09/588,947A
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/130,696
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 60/131,278
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131,673
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/136,784
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,659
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: 60/145,824
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 60/167,239
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 60/168,624
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14

; PRIOR APPLICATION NUMBER: PCT/US96/17957
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-588-947A-30
Query Match 48.4%; Score 582.5; DB 4; Length 219;
Best Local Similarity 54.5%; Pred. No. 1.4e-59;
Matches 127; Conservative 16; Mismatches 25; Indels 65; Gaps 4;
QY 51 YQLAALQADLMNRMELQSYRGSATPAAA-----KLLTPAAPRPHNSS 93
Db 1 YQVAAVQGDLSRAELQSHAEKLPARAPAKAGLGEAPAVTAGLKIFEPPAPGEGNSS 60
QY 94 RGHNRRAFPGPETEEDVDLSAPPALRNIIODCLQLIADSDTPTRKGTTFVFWLLSF 153
Db 61 QSSRNKRAIOGAET-----VIQDCIQLIADSETPTIQKSYTFVFWLLSF 106
QY 154 KRGNAL-----YSQVLYTDPFAMGHVIOKKVHVFGDELSTVTLFRC 196
Db 107 KRGSALKEENKILVKETGYFFIYQVLYTDTKYAMGHLIQKKVHVFGDELSTVTLFRC 166
QY 197 IQN-----LEEGBEIOQLAIAPRENAQISRGDDTFFGALKLL 232
Db 167 IQNMPETLPNNSCYSAGIAKLEEGDELQALAIAPRENAQISLDGDTFFGALKLL 219

RESULT 11
US-09-589-287B-28
; Sequence 28, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/130,696
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 60/131,278
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131,673
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/136,784
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,659
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: 60/145,824
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 60/167,239
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 60/168,624
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14

Query Match 48.0%; Score 578.5; DB 4; Length 219;
Best Local Similarity 54.1%; Pred. No. 1.4e-59;
Matches 126; Conservative 16; Mismatches 26; Indels 65; Gaps 4;
QY 51 YQLAALQADLMNRMELQSYRGSATPAAA-----KLLTPAAPRPHNSS 93
Db 1 YQVAAVQGDLSRAELQSHAEKLPARAPAKAGLGEAPAVTAGLKIFEPPAPGEGNSS 60
QY 94 RGHNRRAFPGPETEEDVDLSAPPALRNIIODCLQLIADSDTPTRKGTTFVFWLLSF 153
Db 61 QSSRNKRAIOGAET-----VIQDCIQLIADSETPTIQKSYTFVFWLLSF 106
QY 154 KRGNAL-----YSQVLYTDPFAMGHVIOKKVHVFGDELSTVTLFRC 196
Db 107 KRGSALKEENKILVKETGYFFIYQVLYTDTKYAMGHLIQKKVHVFGDELSTVTLFRC 166
QY 197 IQN-----LEEGBEIOQLAIAPRENAQISRGDDTFFGALKLL 232
Db 167 IQNMPETLPNNSCYSAGIAKLEEGDELQALAIAPRENAQISLDGDTFFGALKLL 219

RESULT 12
US-09-588-947A-28

Sequence 28, Application US/09588947A
Patent No. 6562579
GENERAL INFORMATION:
APPLICANT: Yu et al.
TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
FILE REFERENCE: PF343P3C2
CURRENT APPLICATION NUMBER: US/09/588,947A
CURRENT FILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: 09/588,947
PRIOR FILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: 09/507,968
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/122,388
PRIOR FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: 60/124,097
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/126,599
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/127,598
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: 60/130,412
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/130,696
PRIOR FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: 60/131,278
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131,673
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 60/136,784
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/142,659
PRIOR FILING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: 60/145,824
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: 60/167,239
PRIOR FILING DATE: 1999-11-24
PRIOR APPLICATION NUMBER: 60/168,624
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 60/171,108
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/171,626
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/176,015
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 09/255,794
PRIOR FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: 09/005,874
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/036,100
PRIOR FILING DATE: 1997-01-14
PRIOR APPLICATION NUMBER: PCT/US96/17957
PRIOR FILING DATE: 1996-10-25
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
US-09-588-947A-28

Query Match 48.0%; Score 578.5; DB 4; Length 219;
Best Local Similarity 54.1%; Pred. No. 4e-59;
Matches 126; Conservative 16; Mismatches 26; Indels 65; Gaps 4;
QY 51 YQLAALQADLNLRLMELQSYRGSAATPAAA-----KLLTPAARPHNS 93
DB 1 YQVAVQGLDASLRAELQGHAEKLPARAPAKGLGEAPAVTAGLKIFEPPAGEGNS 60
QY 94 RGHNRRAFPCCPEETEODVLSAPPALRNIIODCLQIADSDTPTIRKGTTFVFWLASF 153
DB 61 QSSNRKRAIQGAET-----VQDCQLQIADSETPTIQKSGTYTFVFWLUSF 106
QY 154 KRGNAL-----YSQVLYTDPIFAMGHVIQKRVHVFGEDELSTLTPRC 196

Db 107 KRGSALBEKENKILVKETGYFFIYQVLYTDKTYAMGHLIQRKKVHVFGEDELSTLTPRC 166
QY 197 IQN-----LEEGDEIQLAIPRENAQISRNQDDTFFGALKLL 232
DB 167 IQNMPETLPNNSCYSAGIAKLEEGDEIQLAIPRENAQISLDGDTFFGALKLL 219
RESULT 13
US-09-589-287B-19
Sequence 19, Application US/09589287B
Patent No. 6403770
GENERAL INFORMATION:
APPLICANT: Yu et al.
TITLE OF INVENTION: Antibodies to Neutrokin-alpha
FILE REFERENCE: PF343P3C1
CURRENT APPLICATION NUMBER: US/09/589,287B
CURRENT FILING DATE: 2000-06-08
Prior application data removed - check PALM or file wrapper
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 266
TYPE: PRT
ORGANISM: Homo sapiens
US-09-589-287B-19

Query Match 44.1%; Score 531; DB 4; Length 266;
Best Local Similarity 43.7%; Pred. No. 1.8e-53;
Matches 131; Conservative 20; Mismatches 47; Indels 102; Gaps 7;
QY 1 MDESAKTLPPPCLCFCSEKGEDMKV-GYDPTTPPOKRGAV-----LISS 43
DB 1 MDDSTER-EQSLTSLCKKREMKLKECVSLPKRESFVSRSKDGKLLAATLLALLSC 59
QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSAATPAAA-----KLLTPAA 86
DB 60 CLTVSPFYQAALQGLDASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPA 119
QY 87 PRPHNSRGRHNRFAFGPEETEODVLSAPPALRNIIQDCQLQIADSDTPTIRKGTTF 146
DB 120 PEGNSQNRKRAVQGPET-----GSTTF 146
QY 147 VPWLLSEKRGNAL-----YSQVLYTDPIFAMGHVIQKRVHVFGEDEL 189
DB 147 VPWLLSEKRGSALEEKENKILVKETGYFFIYQVLYTDKTYAMGHLIQRKKVHVFGEDEL 206
QY 190 LVTLFRCIQN-----LEEGDEIQLAIPRENAQISRNQDDTFFGALKLL 232
DB 207 LVTLFRCIQNMPETLPNNSCYSAGIAKLEEGDEIQLAIPRENAQISLDGDTFFGALKLL 266

RESULT 14
US-09-879-919-24
Sequence 24, Application US/09879919
Patent No. 6541224
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang, et al.
TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REFERENCE: PF253P1
CURRENT APPLICATION NUMBER: US/09/879,919
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,978
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/254,875
PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 60/241,952
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/211,537


```
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-24

Query Match      44.1%; Score 531; DB 4; Length 266;
Best Local Similarity 43.7%; Pred. No. 1.8e-53;
Matches 131; Conservative 20; Mismatches 47; Indels 102; Gaps 7;

QY 1 MDESATLPPCLPCFCEKEDMKV-GYDPTTPQKEGAV-----LLSS 43
DB 1 MDDSTER-BQSRLTSLCKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSC 59
QY 44 SFTAMSLYQALQADLNLMLQSLYRGSATPAAA-----KLLTPAA 86
DB 60 CLTVSVFYQVAALQGLASRLAEQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPA 119
QY 87 PRPHNSSRGRHNRRAFPFGPEETEODVDLSAPPALRNIIQDCLQIADSDTPTIRKGYTF 146
DB 120 PEGNSSQNSRNKRAVQGPET-----GSYTF 146
QY 147 VPWLLSFRRGNAL-----YSQVLYTDPFAMGHVIOQKKVHVFGDELS 189
DB 147 VPWLLSFRRGSALBEKENILVKETGYFYIYQVLYTKTYAMGHLIQKKVHVFGDELS 206
QY 190 LVTLPFCION-----LEEGDEIQALIPRENAQISRNQDDTFFGALKLL 232
DB 207 LVTLPFCIONMPETLPNNSCYSAGIAKLEEGDELQALIPRENAQISLDGDDVTFFGALKLL 266

RESULT 15
US-09-588-947A-19
; Sequence 19, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C2
; CURRENT APPLICATION NUMBER: US/09/588,947A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/130,696
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 60/131,278
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131,673
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/136,784
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,659
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: 60/145,824
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; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 60/167,239
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 60/168,624
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: PCT/US96/17957
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-588-947A-19

Query Match      44.1%; Score 531; DB 4; Length 266;
Best Local Similarity 43.7%; Pred. No. 1.8e-53;
Matches 131; Conservative 20; Mismatches 47; Indels 102; Gaps 7;

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